REMARKS

1. Information Disclosure Statement

The Examiner notes that the IDS filed March 24, 2004 "contains 2 pages of form PTO-892 from the parent application that have been lined through. This fails to comply with 37 CFR 1.98(a)(1)... The information disclosure statement has been placed in the application file, but the information referred to therein has not been considered".

Our file copy for this case has two pages of 892s from the prior case (one listing Bork the other Witkowski, as the first reference), but neither page has any lined through text (copy enclosed). It therefore seems to us is that if these forms were lined through, it happened at the PTO after we filed this case, and we are not responsible for same.

Moreover, these 892s are clearly compliant (if not lined through by applicant) with 37 CFR 1.98(a)(1). When an IDS is filed with an application, as it was in this case, it is clearly not possible to place, on each page of the IDS, the serial number of the application in which the IDS is being submitted, because the serial number is not yet assigned. The 892 forms in question segregate US patents from citations of other documents, provide a column for the application, and have a heading that clearly indicates that the list is an IDS ("Notice of References Cited").

Without conceding that the 892s were in any way non-compliant, to facilitate prosecution counsel has now added, to the enclosed copies, the words "INFORMATION DISCLOSURE STATEMENT" and the now-known serial number of this case (10/807,115) and requests that the references be considered.

2. Written Description

Claims 1-10 and 12-19 stand rejected under the written description requirement of 35 USC 112, para. 1. We traverse.

Claim 1 is directed to

> 1. An isolated or non-naturally occurring DNA construct, the nucleic acid sequence of which comprises (I) a coding sequence coding for an

> expressible protein which is (a) a pre-prochymosin, prochymosin, or chymosin of a mammal of the suborder Tylopoda or (b) a fusion protein comprising a core protein, wherein said fusion protein is cleavable to release said core protein and wherein said core protein is such a pre-prochymosin, prochymosin or chymosin; and
> (II) appropriate expression signals, operably linked to said coding sequence, permitting the protein to be expressed in a host cell.

Claim 2 limits the mammal to genus Camelus, and claim 3, to the species Camelus dromedaries.

Claim 5 is a method of producing the tylopodal protein encoded by the DNA of claim 1, and is limited by claim 6 to a Camelus dromedaries protein and by claim 19 to the genus Camelus.

Claims 10 and 11 recite

> 10. The method of claim 5 wherein the DNA construct is identical to pGAMpR except that said DNA construct comprises a different coding sequence.
>
> 11. The method of claim 10 wherein the DNA construct is pGAMpR-C as contained in the *Aspergillus niger var.* awamori strains deposited under the accession numbers CBS 108915 and CBS 108916.[1]

The Examiner states

> Suborder of Tylopoda comprises various mammals. The genus of *Camelus* comprises various species including *Camelus dromedaries*. In a given species chymosin can be encoded by single or different genes. (i.e., the claim covers all allelic variants of the chymosin gene in each species).

The Examiner opines that "the claims are drawn to a large highly diverse genus of nucleic acid sequences from Tylopoda, Camelus or Camelus dromedaries encoding pre-prochymosin, prochymosin, or chymosin".

The Examiner concedes that the specification discloses, as

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[1] We have amended 11 to make it dependent on 5, not 10, since 10 expressly is not identical to pGAMpR.

a representative example of the claimed genus of DNA constructs, "a single plasmid pGAMpR-C containing Camelus dromedaries gene coding for chymosin (pages 18-19, Example 1).

The Examiner says that the legal standard for written description is, per Eli Lilly:

> To fully describe a genus of genetic material, which is a chemical compound, applicants must (1) fully describe at least one species of the claimed genus sufficient to represent said genus whereby a skilled artisan, in view of the prior art, could predict the structure of other species encompassed by the claimed genus and (2) identify the common characteristics of the claimed molecules, e.g., structure, physical and/or chemical characteristics, functional characteristics when coupled with a known or disclosed correlation between function and structure, or a combination of these.

We agree with this statement of the law, but believe it has been misapplied here.

We first address the issue of taxonomic diversity. The suborder Tylopoda is divided into four families: Xiphodontidae, Protoceratidae, Oromerycidae, and camelidae. The first three families are extinct and hence are irrelevant to the patentability issues.

The family Camelidae in turn consists of three genera, and a total of six species, as follows

Llama
L. glama (llama)
L. guanicoe (Guanaco)

Vicugna
V. vicugna (Vicuña)
V. pacos (Alpaca)
(formerly classified as L. pacos)

Camelus
C. dromedaries (Dromedary)
C. bactrianus (Bactrian Camel).

We don't think that a taxon consisting of merely six living species (Tylopoda) or two living species (Camelus) can be

considered "diverse", let alone large and, highly diverse, absent some prima facie showing by the examiner.

Prochymosin sequences for the six species in question have not been published, but the inventors have obtained the complete sequences for C. dromedaries, C. bactrianus and L. llama, and a partial sequence for L. guanicoe.

The table below compiles the amino acid identity of these four species with each other and with Bos taurus and water buffalo:

	Bos taurus	water buffalo	C. bactrianus	C. dromedarius	Llama	Guanaco
Bos taurus	100	94	83	84	84	86
water buffalo		100	79	80	80	84
C. bactrianus			100	98	97	96
C. dromedarius				100	98	96
Llama					100	96
Guanaco						100

It can be seen that the tylopodal prochymosins have a sequence identity among themselves which lies in the 98% range, but are only 80-93% identical to Bos taurus, and 79-84% identical to water buffalo.

We respectfully direct the Examiner's attention to the Example 14 in the PTO's Revised Written Description Guideline Training Materials:

> There is actual reduction to practice of the single disclosed species [SEQ ID NO:3]. The specification indicates that the genus of proteins that must be variants of SEQ ID NO: 3 does not have substantial variation since all of the variants must possess the specified catalytic activity and must have at least 95% identity to the reference sequence, SEQ ID NO: 3. The single species disclosed is representative of the genus

> because all members have at least 95% structural identity with the reference compound and because of the presence of an assay which applicant provided for identifying all of the at least 95% identical variants of SEQ ID NO: 3 which are capable of the specified catalytic activity. One of skill in the art would conclude that applicant was in possession of the necessary common attributes possessed by the members of the genus.

While claim 1 doesn't use explicit percentage sequence identity language, it is clear that the tylopodal chymosins in fact share at least 95% sequence identity. The term "chymosin" implies a particular biological activity. Hence, claim 1 is within the purview of RWDGTM Ex. 14.

It is also interesting to note that when these sequences are aligned with each other and bovine chymosin (see Figures A and B attached), there are three areas of special interest:

- a.a. 57-68, with 6 *Tylopoda* specific amino acids. The differences between *Tylopoda* and bovine chymosin in this area result in a remarkable change in charge. These comprise the first amino acids of the mature chymosin molecule.

- a.a 160-161. Two very exposed amino acid residues at the backbone of the molecule.

- a.a 301-329. Most differences between *Tylopoda* and bovine prochymosins are located at the C-terminal part of the molecule. The 301-329 area is located at the entrance of the catalytical cleft and is likely to be responsible for interaction with the casein substrate of the molecule.

Most differences from bovine chymosin are found in all four *Tylopoda* species analyzed. There are only two cases in which both *Camelus* sequences differ from the two *Llama* sequences (in both cases the *Camelus* chymosins have an 'R' while the *Llama* chymosins have H in one case and Q in the other case).

Based on this comparison it is unlikely that major differences will be found in the functional properties of different *Tylopoda* chymosin molecules.

Even absent knowledge of the tylopodal chymosin sequences, it would have been expected that they are similar in structure, given the overall similarity seen for other tylopodal proteins.

There are only a few proteins for which published sequences are available for the three tylopodal genera, Camelus, Llama and Vicugna (see Exs. C-F).

The first is cytochrome b. Using a Camelus dromedarius sequence (P24952) as the query sequence, we found the following BLAST search results (Ex. G)[2]

	Identity	Similarity
C. bactrianus (Q34028)	97	98
L. glama (Q5GH08)	94	97
L. guanicoe (Q5GH04)	94	97
V. vicugna (Q5GH07)	93	96
L. pacos (Q5G115)	93	96
Sus philippensis (Q5BQG9) (highest-ranked non-tylopodal)	90	95

We see that at least the Cameuls genus cytochrome b proteins have within- taxon identity exceeding 95% and the tylopodal proteins generally are at least 93% identical to C. dromedarius. Cytochrome b being a housekeeping protein, it is pretty well conserved even across a broader taxonomic

[2] BLAST search, without low-complexity filtering since that corrupts the percent identity calculation.

distance.

Then we have hemoglobin alpha and beta chain; searching with a C. dromedarius sequence alpha (P63106) (Ex. H) and beta (P68231) (Ex. I) we get:

	vs. C. dromedarius Hemoglobin A chain (P63106)		vs. C. dromedarius Hemoglobin B chain (P68231)	
	Identity	Similarity	Identity	Similarity
C. bactrianus	100 (P63105)	100	100 (P68230)	100
L. pacos	97 (P67816)	99	98 (P68228)	100
L. guanicoe	97 (P67815)	99	98 (P68229)	100
L. vicugna	97 (P07425)	98	98 (P68227)	100
L. glama	96 (P01973)	98	98 (P68226)	100
Colobus badius (best non-tylopodal hit for Hgb-alpha	87 (P01930)	92		
Ailuropoda melanoleuca (best non-tylopodal hit for Hgb-beta)			86 (P18983)	93

Again, we see that the tylopodal globin proteins have within-taxon identities of over 95%.

Additional examples could be provided. While we don't have comparative sequence data on other tylopodal milk proteins it is interesting to note that for alpha-1 casein and beta casein, the best non-tylopodal matches to C. dromedarius have 47% (Ex. J) and 67% (Ex. K) identity, respectively.

Clearly, the art would consider a Camelus dromedarius protein to be representative of its tylopodal homologues.

As to allelic variation of the chymosin gene within the species Camelus dromedaries, the Examiner has not made a prima facie showing that the degree of allelic variation is or would

have been expected to be so great that the particular sequence embodied in pGAMpR-C would not be representative of all C. dromedaries chymosins. In this regard, note that for the proteins for which multiple C. dromedaries isolates have been sequenced, the isolated have all been at least 95% identical, and often completely identical, with the query sequence.

Enablement

1. The Examiner contends that the claims are enabling only for a nucleic acid sequence encoding chymosin contained in pGAMpR-C.

> While recombinant hybridization techniques are known, only highly homologous sequences can be identified using a given sequence. The state of the art provides no reasonable expectation of success in obtaining a nucleic acid sequence from Tylopoda, *Camelus*, or another gene of *Camelus dromedaries* and the result of such screening is unpredictable.

It is clear from the showing made in connection with written description that the tylopodal proteins would have been expected to be highly homologous and are indeed highly homologous.

The literature shows that it is possible to use a gene of one species as a hybridization probe to isolate the homologous gene of another species even when the corresponding proteins have amino acid identities of less than 95%.

For the use of probes to successfully identify homologous genes in other species, see, e.g., Schwinn, et al., J. Biol. Chem., 265:8183-89 (1990) (hamster 67-bp cDNA probe vs. human leukocyte genomic library; human 0.32kb DNA probe vs. bovine brain cDNA library, both with hybridization at 42°C in 6xSSC); Jenkins et al., J. Biol. Chem., 265:19624-31 (1990) (Chicken 770-bp cDNA probe vs. human genomic libraries; hybridization at 40°C in 50% formamide and 5xSSC); Murata et al., J. Exp. Med., 175:341-51 (1992) (1.2-kb mouse cDNA probe v. human

eosinophil cDNA library; hybridization at 65°C in 6xSSC); Guyer et al., J. Biol. Chem., 265:17307-17 (1990) (2.95-kb human genomic DNA probe vs. porcine genomic DNA library; hybridization at 42°C in 5xSSC).

Since the tylopodal proteins have identities exceeding 95% it would not, and indeed did not, require undue experimentation to isolate chymosin genes of C. bactrianus, L. llama and L. guanicoe using the C. dromedaries sequence from pGAMpR-C as a probe. Likewise, it would not require undue experimentation to likewise isolate chymosin genes of V. vicugna or V. pacos.

2. In response to OA page 7, Applicants hereby states for the record that CBS 108915 and 108916 were deposited on June 13, 2000 under the Budapest Treaty, and will be made available in compliance with 37 CFR 1.801-1.809.

Respectfully submitted,

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By:_____
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Enclosures
-copies of previously filed 892s, marked-up as described in section 1 of response
-Figures A and B
-Exhibit C: Camelus bactrianus proteins with known sequences
-Exhibit D: Llama proteins with known sequences
-Exhibit E: Vicugna proteins with known sequences
-Exhibit F: Camelus dromedarius proteins with known sequences
-Exhibits G-K: BLAST search results

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INFORMATION DISCLOSURE STATEMENT ***Notice of References Cited***	Application/Control No. 10/807,115	Applicant(s)/Patent Under Reexamination KAPPELER ET AL.	
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U.S. PATENT DOCUMENTS

*		Document Number Country Code-Number-Kind Code	Date MM-YYYY	Name	Classification
	A	US-			
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	O					
	P					
	Q					
	R					
	S					
	T					

NON-PATENT DOCUMENTS

*		Include as applicable: Author, Title Date, Publisher, Edition or Volume, Pertinent Pages)
	U	Bork , Genome Research, 10:398-400, 2000.
	V	Broun et al. , Science 282:1315-1317, 1998.
	W	Van de Loo et al. , Proc. Natl. Acad. Sci. 92:6743-6747, 1995.
	X	Seffernick et al. , J. Bacteriol. 183(8):2405-2410, 2001.

*A copy of this reference is not being furnished with this Office action. (See MPEP § 707.05(a).)
Dates in MM-YYYY format are publication dates. Classifications may be US or foreign.

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	Q					
	R					
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*		Include as applicable: Author, Title Date, Publisher, Edition or Volume, Pertinent Pages)
	U	Witkowski et al. , Biochemistry 38:11643-11650, 1999.
	V	Nomura et al. , Appl. Microbiol. Biotechnol. 42:865-870, 1995.
	W	Pungercar et al. , Nucleic Acids Research 18(15):4602, 1990
	X	

*A copy of this reference is not being furnished with this Office action. (See MPEP § 707.05(a).)
Dates in MM-YYYY format are publication dates. Classifications may be US or foreign.

Figure A, comparison of bovine prochymosin with prochymosins from different Tylopda species. Aminoacids indicated with bold and blue in the consensus sequence are conserved within the *Tylopoda* family but absent in the bovine family. *Tylopoda* specific sequence motifs with a potential structural function have been underlined in the consensus sequence.

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                                                50
Bos bovis chymosin B      (1) MRCLVVLLAVFALSQGAEITRIPLYKGKSLRKALKEHGLLEDFLQKQQYG
       Water buffalo      (1) ---------------MAEITRIPLCKGKSLRKALKEHGLLEDFLQKQQYG
 Camelus dromedarius      (1) MRCLVVLLAALALSQASGITRIPLHKGKTLRKALKERGLLEDFLQRQQYA
       C. bactrianus      (1) MRCLVVLLAALALSQASGITRIPLHKGKTLRKALKERGLLEDFLQRQQYA
             guanaco      (1) ---------------------IPLYKGKTLRKALKEHGLLEDFLQRQQYA
               Llama      (1) MRCLVVLLAALALSQASGITRIPLYKGKTLRKALKEHGLLEDFLQRQQYA
           Consensus      (1) MRCLVVLLAALALSQASGITRIPLYKGKTLRKALKEHGLLEDFLQRQQYA
                              51                                               100
Bos bovis chymosin B     (51) ISSKYSGFGEVASVPLTNYLDSQYFGKIYLGTPPQEFTVLFDTGSSDFWV
       Water buffalo     (36) VSSKYSGFGEVASVPLTNYLDSQYFGKIYLGTPPQEFTVLFDTGSSDFWV
 Camelus dromedarius     (51) VSSKYSSLGKVAREPLTSYLDSQYFGKIYIGTPPQEFTVVFDTGSSDLWV
       C. bactrianus     (51) VSSKYSSLGKVAREPLTSYLDSQYFGKIYIGTPPQEFTVVFDTGSSDLWV
             guanaco     (30) VSSKYSSLGKVAREPLTSYLDSQYFGKIYIGTPPQEFTVVFDTGSSDLWV
               Llama     (51) VSSKYSSLGKVAREPLTSYLDSQYFGKIYIGTPPQEFTVVFDTGSSDLWV
           Consensus     (51) VSSKYSSLGKVAREPLTSYLDSQYFGKIYIGTPPQEFTVVFDTGSSDLWV
                             101                                              150
Bos bovis chymosin B    (101) PSIYCKSNACKNHQRFDP---RKSSTFQNLGKPLSIHYGTGSMQGILGYD
       Water buffalo     (86) PSIYCKSNACKNHQRFDP---RKSSTFQNLGKPLSIRYGTGSMQGILGYD
 Camelus dromedarius    (101) PSIYCKSNVCKNHHRFDP---RKSSTFRNLGKPLSIHYGTGSMEGFLGYD
       C. bactrianus    (101) PSIYCKSNACKNHHRFDP---RKSSTFRNLGKPLSIHYGTGSIEGFLGYD
             guanaco     (80) PSIYCKSNACXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
               Llama    (101) PSIYCKSNVCKNHHRFDP---RKSSTFRNLGKPLSIHYGTGSMEGFLGYD
           Consensus    (101) PSIYCKSNACKNHHRFDPXXXRKSSTFRNLGKPLSIHYGTGSMEGFLGYD
                             151                                              200
Bos bovis chymosin B    (148) TVTVSNIVDIQQTVGLSTQEPGDVFTYAEFDGILGMAYPSLASEYSIPVF
       Water buffalo    (133) TATVSNIVDIQQTVGLSTQEPGDVFTYAEFDGILGMAYPSLASEYSIPVF
 Camelus dromedarius    (148) TVTVSNIVDPNQTVGLSTEQPGEVFTYSEFDGILGLAYPSLASEYSVPVF
       C. bactrianus    (148) TVTVSNIVDPNQTVGLSTEQPGEVFTYSEFDGILGLAYPSLASEYSVPVF
             guanaco    (130) XXXVSNIVDPNQTVGLSTEQPGEVFTYSEFDGILGLAYPSLASEYSVPVF
               Llama    (148) TVTVSNIVDPNQTVGLSTEQPGEVFTYSEFDGNLGLAYPSLASEYSVPVF
           Consensus    (151) TVTVSNIVDPNQTVGLSTEQPGEVFTYSEFDGILGLAYPSLASEYSVPVF
                             201                                              250
Bos bovis chymosin B    (198) DNMMNRHLVAQDLFSVYMDRNGQESMLTLGAIDPSYYTGSLHWVPVTVQQ
       Water buffalo    (183) DNMMNRHLVAQDLFSVYMDRNGQESMLTLGAIDPSYYTGSLHWVPVTVQQ
 Camelus dromedarius    (198) DNMMDRHLVARDLFSVYMDRNGQGSMLTLGAIDPSYYTGSLHWVPVTLQQ
       C. bactrianus    (198) DNMMDRHLVARDLFSVYMDRNGQGSMLTLGATDPSYYTGSLHWVPVTVQQ
             guanaco    (180) DNMMDRHLVAQDLFSVYMDXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
               Llama    (198) DNMMDRHLVAQDLFSVYMDRNGQGSMLTLGAIDSSYYTGSLHWVPVTVQQ
           Consensus    (201) DNMMDRHLVAQDLFSVYMDRNGQGSMLTLGAIDPSYYTGSLHWVPVTVQQ
                             251                                              300
Bos bovis chymosin B    (248) YWQFTVDSVTISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGAT
       Water buffalo    (233) YWQFTVDSITISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGAT
 Camelus dromedarius    (248) YWQFTVDSVTINGVAVACVGGCQAILDTGTSVLFGPSSDILKIQMAIGAT
       C. bactrianus    (248) YWQVTVDSVTINGVAVACVGGCQAILDTGTSVLFGPSSDILKIQMAIGAT
             guanaco    (230) XXXXXXXXVTINGVAVACVGGCQAILDTGTSVLFGPSSDILKIQMAIGAT
               Llama    (248) YWQVTVDSVTINGVAVACVGGCQAILDTGTSVLFGPSSDILKIQKAIGAT
           Consensus    (251) YWQFTVDSVTINGVAVACVGGCQAILDTGTSVLFGPSSDILKIQMAIGAT
                             301                                              350
Bos bovis chymosin B    (298) QNQYGEFDIDCDNLSYMPTVVFEINGKMYPLTPSAYTSQDQGFCTSGFQS
       Water buffalo    (283) QNQYGEFDIDCDNLSYMPTVVSEINGKMYPLTPSAYTSQDQGFCTSGFQS
 Camelus dromedarius    (298) ENRYGEFDVNCGNLRSMPTVVFEINGRDYPLSPSAYTSKDQGFCTSGFQG
       C. bactrianus    (298) ENRYGEFDVNCGSLRSMPTVVFEINGRDFPLAPSAYTSKDQGFCTSGFQG
             guanaco    (280) ENRYGEFDVNCGNLRSMPTVVFEINGRDFPLAPSAYTSKDQGFCTSGFQS
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Llama	(298)	ENRYGEFDVNCGNLRSMPTVVFEINGRDYPLSPSAYTSKDQGFCTSGFQG
Consensus	(301)	**E**NRYGEFD**VN**C**G**NL**RS**MPTVVFEING**RD**YPLSPSAYTS**K**DQGFCTSGFQS
		351 384
Bos bovis chymosin B	(348)	ENHSQKWILGDVFIREYYSVFDRANNLVGLAKAI
Water buffalo	(333)	ENRSQQWILGDVFIREYYSVFDRANNLVGLAKAI
Camelus dromedarius	(348)	DNNSELWILGDVFIREYYSVFDRANNRVGLAKAI
C. bactrianus	(348)	DNNSELWILGDVFIREYYSVFDRANNRVGLAKAI
guanaco	(330)	ENHSQKWILGDVFIREYYSVFDRANNLVGLAKAI
Llama	(348)	DNNSELWILGDVFIREYYSVFDRANNRVGLAKAI
Consensus	(351)	DNNSQLWILGDVFIREYYSVFDRANNRVGLAKAI

Figure B, Comparison of the amino acid sequence of bovine, porcine and Tylopoda prochymosins

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                                    50
Bos_bovis_chymosin_B  MRCLVVLLAV FALSQGAEIT RIPLYKGKSL RKALKEHGLL EDFLQKQQYG
      C._bactrianus   MRCLVVLLAA LALSQASGIT RIPLHKGKTL RKALKERGLL EDFLQRQQYA
 Camelus_dromedarius  MRCLVVLLAA LALSQASGIT RIPLHKGKTL RKALKERGLL EDFLQRQQYA
                Lama  MRCLVVLLAA LALSQASGIT RIPLYKGKTL RKALKEHGLL EDFLQRQQYA
                 Pig  .IRGRVLLAV LALSQGSGIT RVPLRKGKSL RKELKERGLL EDFLQKQPYA

                51                                                      100
Bos_bovis_chymosin_B  ISSKYSGFGE VASVPLTNYL DSQYFGKIYL GTPPQEFTVL FDTGSSDFWV
      C._bactrianus   VSSKYSSLGK VAREPLTSYL DSQYFGKIYI GTPPQEFTVV FDTGSSDLWV
 Camelus_dromedarius  VSSKYSSLGK VAREPLTSYL DSQYFGKIYI GTPPQEFTVV FDTGSSDLWV
                Lama  VSSKYSSLGK VAREPLTSYL DSQYFGKIYI GTPPQEFTVV FDTGSSDLWV
                 Pig  LSSKYSSFGE VASEPLTNYL DTQYFGKIYI GTPPQEFTVV FDTGSSELWV

               101                                                      150
Bos_bovis_chymosin_B  PSIYCKSNAC KNHQRFDPRK SSTFQNLGKP LSIHYGTGSM QGILGYDTVT
      C._bactrianus   PSIYCKSNAC KNHHRFDPRK SSTFRNLGKP LSIHYGTGSI EGFLGYDTVT
 Camelus_dromedarius  PSIYCKSNVC KNHHRFDPRK SSTFRNLGKP LSIHYGTGSM EGFLGYDTVT
                Lama  PSIYCKSNVC KNHHRFDPRK SSTFRNLGKP LSIHYGTGSM EGFLGYDTVT
                 Pig  PSVYCKSDAC QNHHRFNPSK SSTFQNLDKP LSIQYGTGSI QGFLGYDTVM

               151                                                      200
Bos_bovis_chymosin_B  VSNIVDIQQT VGLSTQEPGD VFTYAEFDGI LGMAYPSLAS EYSIPVFDNM
      C._bactrianus   VSNIVDPNQT VGLSTEQPGE VFTYSEFDGI LGLAYPSLAS EYSVPVFDNM
 Camelus_dromedarius  VSNIVDPNQT VGLSTEQPGE VFTYSEFDGI LGLAYPSLAS EYSVPVFDNM
                Lama  VSNIVDPNQT VGLSTEQPGE VFTYSEFDGN LGLAYPSLAS EYSVPVFDNM
                 Pig  VAGIVDAHQT VGLSTQEPSD IFTYSEFDGI LGLGYPELAS EYTVPVFDNM

               201                                                      250
Bos_bovis_chymosin_B  MNRHLVAQDL FSVYMDRNGQ ESMLTLGAID PSYYTGSLHW VPVTVQQYWQ
      C._bactrianus   MDRHLVARDL FSVYMDRNGQ GSMLTLGATD PSYYTGSLHW VPVTVQQYWQ
 Camelus_dromedarius  MDRHLVARDL FSVYMDRNGQ GSMLTLGAID PSYYTGSLHW VPVTLQQYWQ
                Lama  MDRHLVAQDL FSVYMDRNGQ GSMLTLGAID SSYYTGSLHW VPVTVQQYWQ
                 Pig  MHRHLVAQDL FAVYMSRNDE GSMLTLGAID PSYYTGSLHW VPVTMQLYWQ

               251                                                      300
Bos_bovis_chymosin_B  FTVDSVTISG VVVACEGGCQ AILDTGTSKL VGPSSDILNI QQAIGATQNQ
      C._bactrianus   VTVDSVTING VAVACVGGCQ AILDTGTSVL FGPSSDILKI QMAIGATENR
 Camelus_dromedarius  FTVDSVTING VAVACVGGCQ AILDTGTSVL FGPSSDILKI QMAIGATENR
                Lama  VTVDSVTING VAVACVGGCQ AILDTGTSVL FGPSSDILKI QKAIGATENR
                 Pig  FTVDSVTING VVVACNGGCQ AILDTGTSML AGPSSDILNI QMAIGATESQ

               301                                                      350
Bos_bovis_chymosin_B  YGEFDIDCDN LSYMPTVVFE INGKMYPLTP SAYTSQDQGF CTSGFQSENH
      C._bactrianus   YGEFDVNCGS LRSMPTVVFE INGRDFPLAP SAYTSKDQGF CTSGFQGDNN
 Camelus_dromedarius  YGEFDVNCGN LRSMPTVVFE INGRDYPLSP SAYTSKDQGF CTSGFQGDNN
                Lama  YGEFDVNCGN LRSMPTVVFE INGRDYPLSP SAYTSKDQGF CTSGFQGDNN
                 Pig  YGEFDIDCGS LSSMPTVVFE ISGRMYPLPP SAYTNQDQGF CTSGFQGDSK

               351                                 381
Bos_bovis_chymosin_B  SQKWILGDVF IREYYSVFDR ANNLVGLAKA I
      C._bactrianus   SELWILGDVF IREYYSVFDR ANNRVGLAKA I
 Camelus_dromedarius  SELWILGDVF IREYYSVFDR ANNRVGLAKA I
                Lama  SELWILGDVF IREYYSVFDR ANNRVGLAKA I
                 Pig  SQHWILGVVF IQEYYSVFDR ANNRVGLAKA I
```

Ex.C

Search in UniProt Knowledgebase (Swiss-Prot and TrEMBL) for: camelus bactrianus

UniProtKB/Swiss-Prot Release 51.6 of 06-Feb-2007: 257964 entries

UniProtKB/TrEMBL Release 34.6 of 06-Feb-2007: 3745801 entries

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Enter search terms:
camelus bactrianus
☐ Prefix and append wildcard '*' to words.
Search in: ☑ Swiss-Prot ☑ TrEMBL
new search clear

By default, this search engine searches for complete words only. If you did not find what you expected, and would try to do a substring match, you should perform a new search and select 'prefix and append wildcard to words'.

- Number of documents found in UniProtKB/Swiss-Prot(9) and UniProtKB/TrEMBL(16): **25**
- Note that the selected sequences can be saved to a file to be later retrieved; to do so, go to the bottom of this page.
- For more directed searches, you can use the Advanced search form, or the Sequence Retrieval System SRS

Search in UniProtKB/Swiss-Prot: There are matches to 9 out of 257964 entries

CYB_CAMBA (**Q34028**)
Cytochrome b. {GENE: Name=MT-CYB; Synonyms=COB, CYTB, MTCYB} - Camelus bactrianus (Bactrian camel)
HBA_CAMBA (**P63105**)
Hemoglobin subunit alpha (Hemoglobin alpha chain) (Alpha-globin). {GENE: Name=HBA} - Camelus bactrianus (Bactrian camel)

HBB_CAMBA (**P68230**)
Hemoglobin subunit beta (Hemoglobin beta chain) (Beta-globin). {GENE: Name=HBB} - Camelus bactrianus (Bactrian camel)
IFNG_CAMBA (**Q865W6**)
Interferon gamma precursor (IFN-gamma). {GENE: Name=IFNG} - Camelus bactrianus (Bactrian camel)
IL13_CAMBA (**Q865W5**)
Interleukin-13 precursor (IL-13). {GENE: Name=IL13} - Camelus bactrianus (Bactrian camel)
IL2_CAMBA (**Q2PE47**)
Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF). {GENE: Name=IL2} - Camelus bactrianus (Bactrian camel)
IL6_CAMBA (**Q865W7**)
Interleukin-6 precursor (IL-6). {GENE: Name=IL6} - Camelus bactrianus (Bactrian camel)
RNAS1_CAMBA (**P67929**)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A). {GENE: Name=RNASE1; Synonyms=RNS1} - Camelus bactrianus (Bactrian camel)
TNFA_CAMBA (**Q75N23**)
Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor necrosis factor, membrane form; Tumor necrosis factor, soluble form]. {GENE: Name=TNF; Synonyms=TNFA, TNFSF2} - Camelus bactrianus (Bactrian camel)

Search in UniProtKB/TrEMBL: There are matches to 16 out of 3745801 entries

A1DZ82_CAMBA
Cytochrome b (Fragment) {GENE:Name=cytb} - Camelus bactrianus (Bactrian camel) [Mitochondrion]
A1ILB3_CAMBA
Transcription factor Tbx4 (Fragment) {GENE:Name=TBX4} - Camelus bactrianus (Bactrian camel)
A1ILB4_CAMBA
Transcription factor Tbx4 (Fragment) {GENE:Name=TBX4} - Camelus bactrianus (Bactrian camel)
Q2PE44_CAMBA
Interleukin-10 {GENE:Name=IL-10} - Camelus bactrianus (Bactrian camel)
Q2PE45_CAMBA
Interleukin-4 {GENE:Name=IL-4} - Camelus bactrianus (Bactrian camel)
Q2PE46_CAMBA
Interleukin-12p35 {GENE:Name=IL-12p35} - Camelus bactrianus (Bactrian camel)
Q3KRP3_CAMBA
Cytochrome c oxidase subunit II - Camelus bactrianus (Bactrian camel) [Mitochondrion]
Q540T9_CAMBA
Cytochrome b {GENE:Name=cytb} - Camelus bactrianus (Bactrian camel) [Mitochondrion]

Q68G96_CAMBA
Prion protein {GENE:Name=PrP} - Camelus bactrianus (Bactrian camel)
Q68G98_CAMBA
Prion protein {GENE:Name=PrP} - Camelus bactrianus (Bactrian camel)
Q68G99_CAMBA
Prion protein {GENE:Name=PrP} - Camelus bactrianus (Bactrian camel)
Q865W4_CAMBA
Interleukin 1 alpha (Fragment) {GENE:Name=IL-1 alpha} - Camelus bactrianus (Bactrian camel)
Q8HBR1_CAMBA
Cytochrome b {GENE:Name=cytb} - Camelus bactrianus (Bactrian camel) [Mitochondrion]
Q8HFA7_CAMBA
Cytochrome b {GENE:Name=cytb} - Camelus bactrianus (Bactrian camel) [Mitochondrion]
Q8HFA8_CAMBA
Cytochrome b {GENE:Name=cytb} - Camelus bactrianus (Bactrian camel) [Mitochondrion]
Q9XS40_CAMBA
Ribonuclease X (Fragment) - Camelus bactrianus (Bactrian camel)

If you would like to retrieve all the UniProtKB/Swiss-Prot(9) and UniProtKB/TrEMBL(16) entries contained in this list , you can enter a file name. These entries will then be saved to a file under this name in the directory `outgoing` of the ExPASy anonymous ftp server, from where you can download it. (Please note that this temporary file will only be kept for 1 week.)

File name:

Format: ◉ Swiss-Prot ○ Fasta

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Ex. D

Search in UniProt Knowledgebase (Swiss-Prot and TrEMBL) for: llama

UniProtKB/Swiss-Prot Release 51.6 of 06-Feb-2007: 257964 entries

UniProtKB/TrEMBL Release 34.6 of 06-Feb-2007: 3745801 entries

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Enter search terms:
llama
☐ Prefix and append wildcard '*' to words.
Search in: ☑ Swiss-Prot ☑ TrEMBL
new search clear

By default, this search engine searches for complete words only. If you did not find what you expected, and would try to do a substring match, you should perform a new search and select 'prefix and append wildcard to words'.

- Number of documents found in UniProtKB/Swiss-Prot(23) and UniProtKB/TrEMBL(43): **66**
- Note that the selected sequences can be saved to a file to be later retrieved; to do so, go to the bottom of this page.
- For more directed searches, you can use the Advanced search form, or the Sequence Retrieval System SRS

Search in UniProtKB/Swiss-Prot: There are matches to 23 out of 257964 entries

CYB_LAMGL (**Q34891**)
Cytochrome b. {GENE: Name=MT-CYB; Synonyms=COB, CYTB, MTCYB} - Lama glama (Llama)
FIBA_LAMGL (**P68218**)
Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment). {GENE: Name=FGA} - Lama glama (Llama)
FIBB_LAMGL (**P68122**)
Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment). {GENE: Name=FGB}

- Lama glama (Llama)

HBA_LAMGL (**P01973**)
Hemoglobin subunit alpha (Hemoglobin alpha chain) (Alpha-globin). {GENE: Name=HBA} - Lama glama (Llama)

HBB_LAMGL (**P68226**)
Hemoglobin subunit beta (Hemoglobin beta chain) (Beta-globin). {GENE: Name=HBB} - Lama glama (Llama)

IFNG_CAMBA (**Q865W6**)
Interferon gamma precursor (IFN-gamma). {GENE: Name=IFNG} - Camelus bactrianus (Bactrian camel)

IFNG_LAMGL (**Q865X1**)
Interferon gamma precursor (IFN-gamma). {GENE: Name=IFNG} - Lama glama (Llama)

IL10_LAMGL (**Q865X4**)
Interleukin-10 precursor (IL-10) (Cytokine synthesis inhibitory factor) (CSIF). {GENE: Name=IL10} - Lama glama (Llama)

IL12A_LAMGL (**Q865X0**)
Interleukin-12 subunit alpha precursor (IL-12A) (IL-12 subunit p35) (Cytotoxic lymphocyte maturation factor 35 kDa subunit) (CLMF p35). {GENE: Name=IL12A} - Lama glama (Llama)

IL12B_LAMGL (**Q865W9**)
Interleukin-12 subunit beta precursor (IL-12B) (IL-12 subunit p40) (Cytotoxic lymphocyte maturation factor 40 kDa subunit) (CLMF p40). {GENE: Name=IL12B} - Lama glama (Llama)

IL13_CAMBA (**Q865W5**)
Interleukin-13 precursor (IL-13). {GENE: Name=IL13} - Camelus bactrianus (Bactrian camel)

IL13_LAMGL (**Q865X3**)
Interleukin-13 precursor (IL-13). {GENE: Name=IL13} - Lama glama (Llama)

IL1A_LAMGL (**Q865X7**)
Interleukin-1 alpha precursor (IL-1 alpha). {GENE: Name=IL1A} - Lama glama (Llama)

IL1B_LAMGL (**Q865X8**)
Interleukin-1 beta precursor (IL-1 beta). {GENE: Name=IL1B} - Lama glama (Llama)

IL2_LAMGL (**Q865X2**)
Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF). {GENE: Name=IL2} - Lama glama (Llama)

IL4_LAMGL (**Q865X5**)
Interleukin-4 precursor (IL-4) (B-cell stimulatory factor 1) (BSF-1) (Lymphocyte stimulatory factor 1). {GENE: Name=IL4} - Lama glama (Llama)

IL6_CAMBA (**Q865W7**)
Interleukin-6 precursor (IL-6). {GENE: Name=IL6} - Camelus bactrianus (Bactrian camel)

IL6_LAMGL (**Q865X6**)
Interleukin-6 precursor (IL-6). {GENE: Name=IL6} - Lama glama (Llama)

LCTN_LAMGL (**P83315**)
Lactophorin (Whey protein) (Fragment). - Lama glama (Llama)

NIR_PHOLA (**Q51879**)
Ferredoxin--nitrite reductase (EC 1.7.7.1). {GENE: Name=nirA; Synonyms=nir} - Phormidium laminosum

NRTB_PHOLA (**Q51881**)
Nitrate transport permease protein nrtB. {GENE: Name=nrtB} - Phormidium laminosum
TNFA_LAMGL (**P59694**)
Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor necrosis factor, membrane form; Tumor necrosis factor, soluble form]. {GENE: Name=TNF; Synonyms=TNFA, TNFSF2} - Lama glama (Llama)
TSHB_LAMGL (**P79357**)
Thyrotropin subunit beta precursor (Thyroid-stimulating hormone subunit beta) (TSH-beta) (TSH-B) (Thyrotropin beta chain). {GENE: Name=TSHB} - Lama glama (Llama)

Search in UniProtKB/TrEMBL: There are matches to 43 out of 3745801 entries

A0SMH6_LAMGL
Cytochrome c oxidase subunit III (Fragment) {GENE:Name=COXIII} - Lama glama (Llama) [Mitochondrion]
O97643_LAMGL
Fibrinogen A-alpha chain (Fragment) - Lama glama (Llama)
O97696_LAMGL
Prion protein (Fragment) {GENE:Name=PrP} - Lama glama (Llama)
P79356_LAMGU
Sex-determining protein (Fragment) {GENE:Name=Sry} - Lama guanicoe (Guanaco)
Q3KRP9_LAMGL
Cytochrome c oxidase subunit II - Lama glama (Llama) [Mitochondrion]
Q4F895_RHOER
Aldehyde dehydrogenase {GENE:Name=aldhR} - Rhodococcus erythropolis
Q4ZGZ7_PHOLA
NrtD {GENE:Name=nrtD} - Phormidium laminosum 'OH-1-p Cl 1'
Q4ZGZ8_PHOLA
NrtC {GENE:Name=nrtC} - Phormidium laminosum 'OH-1-p Cl 1'
Q51880_PHOLA
Probable periplasmic protein {GENE:Name=nrtA-Phl} - Phormidium laminosum
Q51882_PHOLA
ATP binding protein {GENE:Name=nrtC-Phl} - Phormidium laminosum
Q7YR06_LAMGL
Apolipoprotein B (Fragment) - Lama glama (Llama)
Q865W4_CAMBA
Interleukin 1 alpha (Fragment) {GENE:Name=IL-1 alpha} - Camelus bactrianus (Bactrian camel)
Q865W8_LAMGL
Beta actin (Fragment) - Lama glama (Llama)
Q8GC77_ERWCH
PagP protein {GENE:Name=pagP} - Erwinia chrysanthemi
Q8GC78_ERWCH
PhoQ protein {GENE:Name=phoQ} - Erwinia chrysanthemi

Q8GC79_ERWCH
PhoP protein {GENE:Name=phoP} - Erwinia chrysanthemi
Q8GCZ3_PHOLA
Global nitrogen control protein (Fragment) {GENE:Name=ntcA} - Phormidium laminosum
Q8W8W9_LAMVI
Cytochrome b (Fragment) - Lama vicugna (Vicugna) (Vicugna vicugna) [Mitochondrion]
Q8W8X0_LAMPA
Cytochrome b (Fragment) - Lama guanicoe pacos (Alpaca) (Lama pacos) [Mitochondrion]
Q8W8X1_LAMGU
Cytochrome b (Fragment) - Lama guanicoe (Guanaco) [Mitochondrion]
Q8W8X2_LAMGL
Cytochrome b (Fragment) - Lama glama (Llama) [Mitochondrion]
Q8WD32_LAMPA
Cytochrome b (Fragment) - Lama guanicoe pacos (Alpaca) (Lama pacos) [Mitochondrion]
Q8WD33_LAMPA
Cytochrome b (Fragment) - Lama guanicoe pacos (Alpaca) (Lama pacos) [Mitochondrion]
Q8WD34_LAMGL
Cytochrome b (Fragment) - Lama glama (Llama) [Mitochondrion]
Q8WD35_LAMGU
Cytochrome b (Fragment) - Lama guanicoe (Guanaco) [Mitochondrion]
Q93KB5_ERWCH
Putative antibiotic biosynthesis protein {GENE:Name=pab} - Erwinia chrysanthemi
Q93KB6_ERWCH
Putative ABC transporter {GENE:Name=ybit} - Erwinia chrysanthemi
Q9BDS1_LAMGL
Recombination activating protein 2 (Fragment) {GENE:Name=rag2} - Lama glama (Llama)
Q9BDS2_LAMGL
Recombination activating protein 1 {GENE:Name=rag1} - Lama glama (Llama)
Q9BDV2_LAMGL
BRCA1 (Fragment) - Lama glama (Llama)
Q9BEJ5_LAMGL
Zinc finger protein ZFX (Fragment) {GENE:Name=ZFX} - Lama glama (Llama)
Q9BEN3_LAMGL
Tyrosinase (Fragment) {GENE:Name=TYR} - Lama glama (Llama)
Q9BES5_LAMGL
Recombination activating protein 2 (Fragment) {GENE:Name=RAG2} - Lama glama (Llama)
Q9BEW8_LAMGL
Recombination activating protein 1 (Fragment) {GENE:Name=RAG1} - Lama glama (Llama)
Q9BF09_LAMGL
Prepronociceptin (Fragment) {GENE:Name=PNOC} - Lama glama (Llama)
Q9BFD4_LAMGL
Cannabinoid receptor 1 (Fragment) {GENE:Name=CNR1} - Lama glama (Llama)

Q9BFI2_LAMGL
Brain-derived neurotrophic factor (Fragment) {GENE:Name=BDNF} - Lama glama (Llama)
Q9BFM8_LAMGL
ATP7A (Fragment) {GENE:Name=ATP7A} - Lama glama (Llama)
Q9BFS6_LAMGL
Amyloid beta protein (Fragment) {GENE:Name=APP} - Lama glama (Llama)
Q9BFX3_LAMGL
Beta-2 adrenergic receptor (Fragment) {GENE:Name=ADRB2} - Lama glama (Llama)
Q9BG17_LAMGL
Adenosine A3 receptor (Fragment) {GENE:Name=ADORA3} - Lama glama (Llama)
Q9XSA4_LAMGL
Von Willebrand factor (Fragment) {GENE:Name=vWF} - Lama glama (Llama)
Q9XSA5_LAMGL
Interphotoreceptor retinoid binding protein (Fragment) {GENE:Name=IRBP} - Lama glama (Llama)

If you would like to retrieve all the UniProtKB/Swiss-Prot(23) and UniProtKB/TrEMBL(43) entries contained in this list , you can enter a file name. These entries will then be saved to a file under this name in the directory `outgoing` of the ExPASy anonymous ftp server, from where you can download it. (Please note that this temporary file will only be kept for 1 week.)

File name:

Format: ◉ Swiss-Prot ○ Fasta

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Ex E

Search in UniProt Knowledgebase (Swiss-Prot and TrEMBL) for: vicugna

UniProtKB/Swiss-Prot Release 51.6 of 06-Feb-2007: 257964 entries

UniProtKB/TrEMBL Release 34.6 of 06-Feb-2007: 3745801 entries

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Enter search terms:
vicugna
☐ Prefix and append wildcard '*' to words.
Search in: ☑ Swiss-Prot ☑ TrEMBL
new search clear

By default, this search engine searches for complete words only. If you did not find what you expected, and would try to do a substring match, you should perform a new search and select 'prefix and append wildcard to words'.

- Number of documents found in UniProtKB/Swiss-Prot(6) and UniProtKB/TrEMBL(5): **11**
- Note that the selected sequences can be saved to a file to be later retrieved; to do so, go to the bottom of this page.
- For more directed searches, you can use the Advanced search form, or the Sequence Retrieval System SRS

Search in UniProtKB/Swiss-Prot: There are matches to 6 out of 257964 entries

CYB_LAMVI (**Q36227**)
Cytochrome b. {GENE: Name=MT-CYB; Synonyms=COB, CYTB, MTCYB} - Lama vicugna (Vicugna) (Vicugna vicugna)
FIBA_LAMVI (**P68219**)
Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment). {GENE: Name=FGA} - Lama vicugna (Vicugna) (Vicugna vicugna)
FIBB_LAMVI (**P68124**)
Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment). {GENE: Name=FGB}

- Lama vicugna (Vicugna) (Vicugna vicugna)

HBA_LAMPA (**P67816**)
Hemoglobin subunit alpha (Hemoglobin alpha chain) (Alpha-globin). {GENE: Name=HBA} - Lama guanicoe pacos (Alpaca) (Lama pacos)

HBA_LAMVI (**P07425**)
Hemoglobin subunit alpha (Hemoglobin alpha chain) (Alpha-globin). {GENE: Name=HBA} - Lama vicugna (Vicugna) (Vicugna vicugna)

HBB_LAMVI (**P68227**)
Hemoglobin subunit beta (Hemoglobin beta chain) (Beta-globin). {GENE: Name=HBB} - Lama vicugna (Vicugna) (Vicugna vicugna)

Search in UniProtKB/TrEMBL: There are matches to 5 out of 3745801 entries

A0SMH8_LAMVI
Cytochrome c oxidase subunit III (Fragment) {GENE:Name=COXIII} - Lama vicugna (Vicugna) (Vicugna vicugna) [Mitochondrion]

Q206M5_LAMVI
Urokinase-type plasminogen activator (Fragment) - Lama vicugna (Vicugna) (Vicugna vicugna)

Q3KRP6_LAMVI
Cytochrome c oxidase subunit II - Lama vicugna (Vicugna) (Vicugna vicugna) [Mitochondrion]

Q5GH07_LAMVI
Cytochrome b {GENE:Name=cytb} - Vicugna vicugna mensalis [Mitochondrion]

Q8W8W9_LAMVI
Cytochrome b (Fragment) - Lama vicugna (Vicugna) (Vicugna vicugna) [Mitochondrion]

If you would like to retrieve all the UniProtKB/Swiss-Prot(6) and UniProtKB/TrEMBL(5) entries contained in this list , you can enter a file name. These entries will then be saved to a file under this name in the directory `outgoing` of the ExPASy anonymous ftp server, from where you can download it. (Please note that this temporary file will only be kept for 1 week.)

File name:

Format: ◉ Swiss-Prot ○ Fasta

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Ex-F

Search in UniProt Knowledgebase (Swiss-Prot and TrEMBL) for: camelus dromedarius

UniProtKB/Swiss-Prot Release 51.6 of 06-Feb-2007: 257964 entries

UniProtKB/TrEMBL Release 34.6 of 06-Feb-2007: 3745801 entries

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Enter search terms:
camelus dromedarius
☐ Prefix and append wildcard '*' to words.
Search in: ☑ Swiss-Prot ☑ TrEMBL
new search clear

By default, this search engine searches for complete words only. If you did not find what you expected, and would try to do a substring match, you should perform a new search and select 'prefix and append wildcard to words'.

- Number of documents found in UniProtKB/Swiss-Prot(29) and UniProtKB/TrEMBL(26): **55**
- Note that the selected sequences can be saved to a file to be later retrieved; to do so, go to the bottom of this page.
- For more directed searches, you can use the Advanced search form, or the Sequence Retrieval System SRS

Search in UniProtKB/Swiss-Prot: There are matches to 29 out of 257964 entries

ACTB_CAMDR (**P84336**)
Actin, cytoplasmic 1 (Beta-actin). {GENE: Name=ACTB} - Camelus dromedarius (Dromedary) (Arabian camel)
CASA1_CAMDR (**O97943**)
Alpha-S1-casein precursor. {GENE: Name=CSN1S1} - Camelus dromedarius (Dromedary) (Arabian camel)

CASA2_CAMDR (**O97944**)
Alpha-S2-casein precursor. {GENE: Name=CSN1S2} - Camelus dromedarius (Dromedary) (Arabian camel)
CASB_CAMDR (**Q9TVD0**)
Beta-casein precursor. {GENE: Name=CSN2} - Camelus dromedarius (Dromedary) (Arabian camel)
CASK_CAMDR (**P79139**)
Kappa-casein precursor. {GENE: Name=CSN3; Synonyms=CSN10, CSNK} - Camelus dromedarius (Dromedary) (Arabian camel)
CFDP1_CAMDR (**Q4ADK7**)
Craniofacial development protein 1 (Bucentaur). {GENE: Name=CFDP1; Synonyms=BCNT} - Camelus dromedarius (Dromedary) (Arabian camel)
COLI_CAMDR (**P01203**)
Beta-endorphin [Contains: Met-enkephalin]. - Camelus dromedarius (Dromedary) (Arabian camel)
CRYAA_CAMDR (**P02472**)
Alpha crystallin A chain [Contains: Alpha crystallin A chain, short form]. {GENE: Name=CRYAA} - Camelus dromedarius (Dromedary) (Arabian camel)
CYB_CAMDR (**P24952**)
Cytochrome b. {GENE: Name=MT-CYB; Synonyms=COB, CYTB, MTCYB} - Camelus dromedarius (Dromedary) (Arabian camel)
CYC_CAMDR (**P68099**)
Cytochrome c. {GENE: Name=CYCS; Synonyms=CYC} - Camelus dromedarius (Dromedary) (Arabian camel)
FIBA_CAMDR (**P14444**)
Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment). {GENE: Name=FGA} - Camelus dromedarius (Dromedary) (Arabian camel)
FIBB_CAMDR (**P68123**)
Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment). {GENE: Name=FGB} - Camelus dromedarius (Dromedary) (Arabian camel)
GLUC_CAMDR (**P68273**)
Glucagon. {GENE: Name=GCG} - Camelus dromedarius (Dromedary) (Arabian camel)
HBA_CAMDR (**P63106**)
Hemoglobin subunit alpha (Hemoglobin alpha chain) (Alpha-globin). {GENE: Name=HBA} - Camelus dromedarius (Dromedary) (Arabian camel)
HBB_CAMDR (**P68231**)
Hemoglobin subunit beta (Hemoglobin beta chain) (Beta-globin). {GENE: Name=HBB} - Camelus dromedarius (Dromedary) (Arabian camel)
INS_CAMDR (**P01320**)
Insulin [Contains: Insulin B chain; Insulin A chain]. {GENE: Name=INS} - Camelus dromedarius (Dromedary) (Arabian camel)
LALBA_CAMDR (**P00710**)
Alpha-lactalbumin (Lactose synthase B protein). {GENE: Name=LALBA} - Camelus dromedarius (Dromedary) (Arabian camel)
LCTN_CAMDR (**P15522**)
Lactophorin precursor (Whey protein) (Proteose-peptone component 3) (PP3). - Camelus dromedarius (Dromedary) (Arabian camel)
LCTN_LAMGL (**P83315**)
Lactophorin (Whey protein) (Fragment). - Lama glama (Llama)

LYSC_CAMDR (**P37712**)
Lysozyme C (EC 3.2.1.17) (1,4-beta-N-acetylmuramidase). {GENE: Name=LYZ} - Camelus dromedarius (Dromedary) (Arabian camel)
MLA_CAMDR (**P61281**)
Melanotropin alpha (Alpha-MSH). - Camelus dromedarius (Dromedary) (Arabian camel)
PGRP_CAMDR (**Q9GK12**)
Peptidoglycan recognition protein precursor (Peptidoglycan recognition protein short) (PGRP-S). {GENE: Name=PGLYRP1; Synonyms=PGLYRP, PGRP} - Camelus dromedarius (Dromedary) (Arabian camel)
PRIO_CAMDR (**P79141**)
Major prion protein precursor (PrP) (CD230 antigen). {GENE: Name=PRNP; Synonyms=PRP} - Camelus dromedarius (Dromedary) (Arabian camel)
PRL_CAMDR (**P22393**)
Prolactin (PRL). {GENE: Name=PRL} - Camelus dromedarius (Dromedary) (Arabian camel)
RNAS1_CAMDR (**P67928**)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A). {GENE: Name=RNASE1; Synonyms=RNS1} - Camelus dromedarius (Dromedary) (Arabian camel)
SOMA_CAMDR (**Q7YRR6**)
Somatotropin precursor (Growth hormone). {GENE: Name=GH1; Synonyms=GH} - Camelus dromedarius (Dromedary) (Arabian camel)
TRFL_CAMDR (**Q9TUM0**)
Lactotransferrin precursor (EC 3.4.21.-) (Lactoferrin). {GENE: Name=LTF} - Camelus dromedarius (Dromedary) (Arabian camel)
UBIQ_CAMDR (**Q865C5**)
Ubiquitin. - Camelus dromedarius (Dromedary) (Arabian camel)
WAP_CAMDR (**P09837**)
Whey acidic protein (WAP). {GENE: Name=WAP} - Camelus dromedarius (Dromedary) (Arabian camel)

Search in UniProtKB/TrEMBL: There are matches to 26 out of 3745801 entries

O02677_CAMDR
Gamma fibrinogen (Fragment) - Camelus dromedarius (Dromedary) (Arabian camel)
Q1RP86_CAMDR
Tyrosine kinase receptor 2 (Fragment) {GENE:Name=tie2} - Camelus dromedarius (Dromedary) (Arabian camel)
Q1RP87_CAMDR
Vascular endothelial growth factor isoform 121 (Fragment) {GENE:Name=vegf} - Camelus dromedarius (Dromedary) (Arabian camel)
Q1RP88_CAMDR
Progesterone receptor (Fragment) {GENE:Name=pr} - Camelus dromedarius (Dromedary) (Arabian camel)
Q1RP89_CAMDR
Estrogen receptor alpha (Fragment) {GENE:Name=er alpha} - Camelus

dromedarius (Dromedary) (Arabian camel)
Q28229_CAMDR
B-casein (Fragment) - Camelus dromedarius (Dromedary) (Arabian camel)
Q28231_CAMDR
Estrogen receptor (Fragment) {GENE:Name=ER} - Camelus dromedarius (Dromedary) (Arabian camel)
Q2KN22_CAMDR
Neonatal Fc receptor alpha-chain {GENE:Name=FCGRT} - Camelus dromedarius (Dromedary) (Arabian camel)
Q3KRP2_CAMDR
Cytochrome c oxidase subunit II - Camelus dromedarius (Dromedary) (Arabian camel) [Mitochondrion]
Q6L7Z3_CAMDR
B-type natriuretic peptide precursor {GENE:Name=BNP} - Camelus dromedarius (Dromedary) (Arabian camel)
Q6L7Z4_CAMDR
Atrial natriuretic peptide precursor {GENE:Name=ANP} - Camelus dromedarius (Dromedary) (Arabian camel)
Q864E3_CAMDR
Recombination activating protein 1 (Fragment) {GENE:Name=RAG-1} - Camelus dromedarius (Dromedary) (Arabian camel)
Q864U9_CAMDR
Leptin receptor long isoform (Fragment) - Camelus dromedarius (Dromedary) (Arabian camel)
Q864V0_CAMDR
Leptin receptor short isoform (Fragment) - Camelus dromedarius (Dromedary) (Arabian camel)
Q864V1_CAMDR
Leptin (Fragment) - Camelus dromedarius (Dromedary) (Arabian camel)
Q8HB83_CAMDR
Cytochrome b {GENE:Name=cytb} - Camelus dromedarius (Dromedary) (Arabian camel) [Mitochondrion]
Q8HBG5_CAMDR
Cytochrome b {GENE:Name=cytb} - Camelus dromedarius (Dromedary) (Arabian camel) [Mitochondrion]
Q8HZ65_CAMDR
Presenilin-1 (Fragment) - Camelus dromedarius (Dromedary) (Arabian camel)
Q8WMP6_CAMDR
Alpha-lactalbumin (Fragment) {GENE:Name=lalba} - Camelus dromedarius (Dromedary) (Arabian camel)
Q9GJW6_CAMDR
Peroxidase precursor (EC 1.11.1.7) {GENE:Name=lactoperoxidase} - Camelus dromedarius (Dromedary) (Arabian camel)
Q9GK10_CAMDR
Pepsin A precursor (EC 3.4.23.1) {GENE:Name=pepsin} - Camelus dromedarius (Dromedary) (Arabian camel)
Q9GK11_CAMDR
Chymosin precursor (EC 3.4.23.4) {GENE:Name=chymosin} - Camelus dromedarius (Dromedary) (Arabian camel)
Q9N0T9_CAMDR

Preprorelaxin - Camelus dromedarius (Dromedary) (Arabian camel)
Q9TS81_CAMDR
Glycerol ester HYDROLAS (EC 3.1.1.3) (Fragments) - Camelus dromedarius (Dromedary) (Arabian camel)
Q9TV02_CAMDR
Prion protein (Fragment) {GENE:Name=PrP} - Camelus dromedarius (Dromedary) (Arabian camel)
Q9TVB7_CAMDR
Pancreatic ribonuclease (EC 3.1.27.5) (Fragment) - Camelus dromedarius (Dromedary) (Arabian camel)

If you would like to retrieve all the UniProtKB/Swiss-Prot(29) and UniProtKB/TrEMBL(26) entries contained in this list , you can enter a file name. These entries will then be saved to a file under this name in the directory `outgoing` of the ExPASy anonymous ftp server, from where you can download it. (Please note that this temporary file will only be kept for 1 week.)

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NCBI BLAST program reference [PMID:9254694]:
Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W.,
Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein
database search programs. Nucleic Acids Res. 25:3389-3402(1997).

==========

Query: 379 AA
Date run: 2007-02-15 21:49:25 UTC+0100 on blast01.vital-it.ch
Program: NCBI BLASTP 2.2.15 [Oct-15-2006]
Database: UniProtKB Mammalia
240,475 sequences; 91,865,493 total letters
UniProt Knowledgebase Release 9.6 consists of:
UniProtKB/Swiss-Prot Release 51.6 of 06-Feb-2007: 257964 entries
UniProtKB/TrEMBL Release 34.6 of 06-Feb-2007: 3745801 entries

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List of potentially matching sequences

Send selected sequences to Clustal W (multiple alignment) Submit Query Select up to...

☐ Include query sequence

	Db AC	Description	Score	E-value
☐	sp P24952	CYB_CAMDR Cytochrome b [MT-CYB] [Camelus dromedarius (...	776	0.0
☐	tr Q8HB83	_CAMDR Cytochrome b [cytb] [Camelus dromedarius (Dromed...	775	0.0
☐	tr Q8HBG5	_CAMDR Cytochrome b [cytb] [Camelus dromedarius (Dromed...	773	0.0
☐	sp Q34028	CYB_CAMBA Cytochrome b [MT-CYB] [Camelus bactrianus (B...	763	0.0
☐	tr Q540T9	_CAMBA Cytochrome b [cytb] [Camelus bactrianus (Bactria...	763	0.0
☐	tr Q8HFA8	_CAMBA Cytochrome b [cytb] [Camelus bactrianus (Bactria...	759	0.0
☐	tr Q8HBR1	_CAMBA Cytochrome b [cytb] [Camelus bactrianus (Bactria...	754	0.0
☐	tr Q8HFA7	_CAMBA Cytochrome b [cytb] [Camelus bactrianus (Bactria...	753	0.0
☐	tr Q5GH08	_LAMPA Cytochrome b [cytb] [Lama glama argentina]	747	0.0
☐	sp Q36227	CYB_LAMVI Cytochrome b [MT-CYB] [Lama vicugna (Vicugna...	745	0.0
☐	sp Q34891	CYB_LAMGL Cytochrome b [MT-CYB] [Lama glama (Llama)]	745	0.0
☐	tr Q5GH03	_LAMGU Cytochrome b [cytb] [Lama guanicoe huanacus]	745	0.0
☐	tr Q5GH04	_LAMGU Cytochrome b [cytb] [Lama guanicoe cacsilensis]	745	0.0
☐	tr Q70LJ9	_LAMPA Cytochrome b [cytb] [Lama guanicoe pacos (Alpaca...	745	0.0
☐	sp Q34916	CYB_LAMPA Cytochrome b [MT-CYB] [Lama guanicoe pacos (...	744	0.0
☐	tr Q5GH09	_LAMPA,Cytochrome b [cytb] [Lama glama chaku]	744	0.0
☐	tr Q5GH11	_LAMPA Cytochrome b [cytb] [Lama pacos suri]	744	0.0
☐	tr Q5GH06	_LAMGU Cytochrome b [cytb] [Lama guanicoe cacsilensis]	743	0.0
☐	sp Q34890	CYB_LAMGU Cytochrome b [MT-CYB] [Lama guanicoe (Guanaco)]	742	0.0
☐	tr Q5GH02	_LAMGU Cytochrome b [cytb] [Lama guanicoe huanacus]	742	0.0
☐	tr Q5GGY6	_LAMGU Cytochrome b [cytb] [Lama guanicoe guanicoe]	742	0.0
☐	tr Q5GH05	_LAMGU Cytochrome b [cytb] [Lama guanicoe cacsilensis]	742	0.0
☐	tr Q5GGY0	_LAMGU Cytochrome b [cytb] [Lama guanicoe guanicoe]	741	0.0
☐	tr O03364	_LAMGU Cytochrome b [Lama guanicoe (Guanaco)]	741	0.0
☐	tr Q5GGZ3	_LAMGU Cytochrome b [cytb] [Lama guanicoe huanacus]	741	0.0
☐	tr Q5GGY2	_LAMGU Cytochrome b [cytb] [Lama guanicoe guanicoe]	741	0.0
☐	tr Q5GGZ7	_LAMGU Cytochrome b [cytb] [Lama guanicoe huanacus]	740	0.0
☐	tr Q5GH07	_LAMVI Cytochrome b [cytb] [Vicugna vicugna mensalis]	739	0.0
☐	tr Q5GGY8	_LAMGU Cytochrome b [cytb] [Lama guanicoe huanacus]	739	0.0
☐	tr Q5GGY9	_LAMGU Cytochrome b [cytb] [Lama guanicoe huanacus]	738	0.0
☐	sp Q5BQG9	CYB_SUSPH Cytochrome b [MT-CYB] [Sus philippensis (Phi...	723	0.0

☐	tr Q9TGH5 _TRAST Cytochrome b [cytb] [Tragelaphus strepsiceros (G...	723	0.0
☐	tr Q5MG70 _PIG Cytochrome b [CYTB] [Sus scrofa coreanus]	722	0.0
☐	tr Q079P0 _PIG Cytochrome b [CYTB] [Sus scrofa (Pig)]	722	0.0
☐	tr Q85C79 _PIG Cytochrome b [cytb] [Sus scrofa (Pig)]	721	0.0
☐	tr Q5MG66 _PIG Cytochrome b [CYTB] [Sus scrofa coreanus]	721	0.0
☐	tr Q1HBG9 _PIG Cytochrome b [cytb] [Sus scrofa (Pig)]	721	0.0
☐	tr Q2NNJ5 _PIG Cytochrome b [CYTB] [Sus scrofa (Pig)]	721	0.0
☐	tr Q5MG65 _PIG Cytochrome b [CYTB] [Sus scrofa coreanus]	721	0.0
☐	tr Q9MEH8 _LAMPA Cytochrome b [Cyt b] [Lama guanicoe pacos (Alpac...	721	0.0
☐	tr Q9XP71 _BOSMU Cytochrome b [cytb] [Bos mutus grunniens (Wild y...	721	0.0
☐	tr Q36543 _SUSBA Cytochrome b [cytb] [Sus barbatus (Bearded pig)]	721	0.0
☐	tr Q1PGA9 _PIG Cytochrome b [Sus scrofa (Pig)]	721	0.0
☐	tr Q9T567 _PIG Cytochrome b [cytb] [Sus scrofa (Pig)]	720	0.0
☐	tr Q5MG74 _PIG Cytochrome b [CYTB] [Sus scrofa coreanus]	720	0.0
☐	tr Q5MG73 _PIG Cytochrome b [CYTB] [Sus scrofa coreanus]	720	0.0
☐	tr Q5MG68 _PIG Cytochrome b [CYTB] [Sus scrofa coreanus]	720	0.0
☐	sp P24964 CYB_PIG Cytochrome b [MT-CYB] [Sus scrofa (Pig)]	720	0.0
☐	sp Q5Y4Q0 CYB_BOSMU Cytochrome b [MT-CYB] [Bos mutus grunniens (...	720	0.0
☐	tr A1X8W9 _PIG Cytochrome b [Sus scrofa (Pig)]	720	0.0
☐	tr Q9T566 _PIG Cytochrome b [cytb] [Sus scrofa (Pig)]	720	0.0
☐	tr Q5MG60 _PIG Cytochrome b [CYTB] [Sus scrofa (Pig)]	720	0.0
☐	tr Q5MG53 _PIG Cytochrome b [CYTB] [Sus scrofa (Pig)]	720	0.0
☐	tr Q5BQG5 _PIG Cytochrome b [cytb] [Sus scrofa (Pig)]	720	0.0
☐	tr Q9T4J0 _PIG Cytochrome b [cytb] [Sus scrofa (Pig)]	719	0.0
☐	tr Q6GV90 _PIG Cytochrome b [CYTB] [Sus scrofa (Pig)]	719	0.0
☐	tr Q9T9B4 _TRAST Cytochrome b [cytb] [Tragelaphus strepsiceros (G...	719	0.0
☐	tr Q1PGA7 _PIG Cytochrome b [Sus scrofa (Pig)]	719	0.0
☐	tr Q8M702 _SUSBA Cytochrome b [cyt-B] [Sus barbatus (Bearded pig)]	719	0.0
☐	tr Q9T568 _PIG Cytochrome b [cytb] [Sus scrofa (Pig)]	719	0.0
☐	tr Q5MG71 _PIG Cytochrome b [CYTB] [Sus scrofa coreanus]	719	0.0
☐	tr P92736 _SYNCA Cytochrome b [Syncerus caffer (Cape buffalo)]	719	0.0
☐	sp Q5J1T5 CYB_SUSCL Cytochrome b [MT-CYB] [Sus celebensis (Celeb...	719	0.0
☐	sp Q8M706 CYB_PHAAF Cytochrome b [MT-CYB] [Phacochoerus africanu...	719	0.0
☐	tr Q5J1T7 _PIG Cytochrome b [cytb] [Sus scrofa (Pig)]	719	0.0
☐	tr Q71KJ5 _PIG Cytochrome b [CYTB] [Sus scrofa (Pig)]	719	0.0
☐	tr Q1WEZ9 _PIG Cytochrome b [CYTB] [Sus scrofa (Pig)]	719	0.0
☐	sp Q8M703 CYB_SUSBA Cytochrome b [MT-CYB] [Sus barbatus (Bearded...	718	0.0
☐	tr Q58FM1 _BOSMU Cytochrome b [cytb] [Bos grunniens mutus]	718	0.0
☐	tr Q5MG76 _PIG Cytochrome b [CYTB] [Sus scrofa coreanus]	718	0.0
☐	tr Q1PGA8 _PIG Cytochrome b [Sus scrofa (Pig)]	718	0.0
☐	tr Q5MG67 _PIG Cytochrome b [CYTB] [Sus scrofa coreanus]	718	0.0
☐	tr Q5MG63 _PIG Cytochrome b [CYTB] [Sus scrofa (Pig)]	718	0.0
☐	sp Q9T9C0 CYB_TETQU Cytochrome b [MT-CYB] [Tetracerus quadricorn...	717	0.0
☐	sp Q9T7T9 CYB_TAPIN Cytochrome b [MT-CYB] [Tapirus indicus (Asia...	717	0.0
☐	sp Q5J1T4 CYB_POTPR Cytochrome b [MT-CYB] [Potamochoerus porcus ...	717	0.0
☐	sp Q5J1T3 CYB_POTLA Cytochrome b [MT-CYB] [Potamochoerus larvatu...	717	0.0
☐	tr Q575Z9 _BOVIN Cytochrome b [Cytb] [Bos taurus (Bovine)]	717	0.0
☐	tr Q5MG61 _PIG Cytochrome b [CYTB] [Sus scrofa (Pig)]	717	0.0
☐	tr Q85QJ9 _PIG Cytochrome b [cytb] [Sus scrofa (Pig)]	717	0.0
☐	tr Q5EG31 _BOVIN Cytochrome b [Bos taurus (Bovine)]	717	0.0
☐	sp Q9TG16 CYB_TRAAN Cytochrome b [MT-CYB] [Tragelaphus angasii (...	717	0.0
☐	sp P48665 CYB_HORSE Cytochrome b [MT-CYB] [Equus caballus (Horse)]	717	0.0
☐	sp P00157 CYB_BOVIN Cytochrome b [MT-CYB] [Bos taurus (Bovine)]	717	0.0
☐	sp Q8HCJ4 CYB_BOSIN Cytochrome b [MT-CYB] [Bos indicus (Zebu)]	717	0.0
☐	tr Q85AW1 _PIG Cytochrome b [cytb] [Sus scrofa (Pig)]	717	0.0
☐	tr Q7JAR2 _BOVIN Cytochrome b [cytb] [Bos taurus (Bovine)]	717	0.0
☐	tr Q5MG50 _PIG Cytochrome b [CYTB] [Sus scrofa (Pig)]	717	0.0
☐	tr Q5EG37 _BOVIN Cytochrome b [Bos taurus (Bovine)]	717	0.0
☐	tr Q53YR5 _HORSE Cytochrome B [CYTB] [Equus caballus (Horse)]	717	0.0
☐	tr Q9T565 _PIG Cytochrome b [cytb] [Sus scrofa (Pig)]	717	0.0
☐	tr Q6GV93 _PIG Cytochrome b [CYTB] [Sus scrofa (Pig)]	717	0.0
☐	tr Q5MG75 _PIG Cytochrome b [CYTB] [Sus scrofa coreanus]	717	0.0
☐	tr Q38J93 _EQUPR Cytochrome b [CYTB] [Equus caballus przewalskii ...	717	0.0
☐	tr Q079R6 _PIG Cytochrome b [CYTB] [Sus scrofa (Pig)]	717	0.0
☐	tr Q3L5V2 _BOVIN Cytochrome b [CYTB] [Bos taurus (Bovine)]	717	0.0
☐	tr O20405 _FELCA Cytochrome b [Felis silvestris catus (Cat)]	717	0.0

☐	tr Q69GE8 _PIG Cytochrome b [CYTB] [Sus scrofa (Pig)]	717	0.0
☐	tr Q5EG28 _BOVIN Cytochrome b [CYTB] [Bos taurus (Bovine)]	717	0.0
☐	tr Q45M48 _BOVIN Cytochrome b [CYTB] [Bos taurus (Bovine)]	717	0.0

Graphical overview of the alignments

Click here to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs
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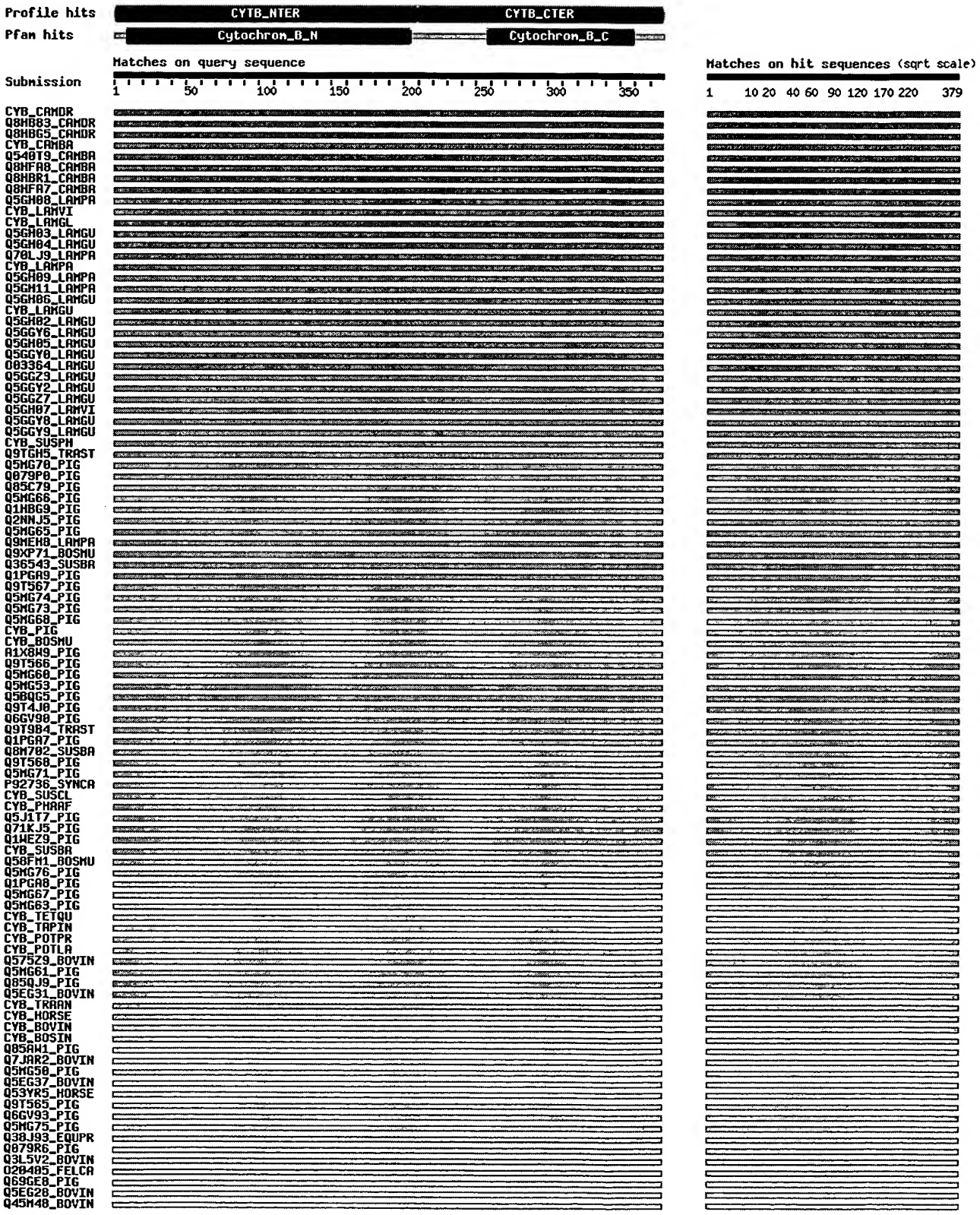

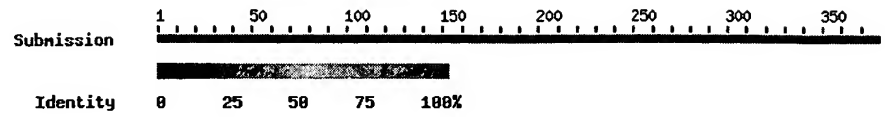

Alignments

sp P24952 CYB_CAMDR **Cytochrome b [MT-CYB] [Camelus dromedarius (Dromedary) (Arabian camel)]** 379 AA align

Score = 776 bits (2004), Expect = 0.0
Identities = 379/379 (100%), Positives = 379/379 (100%)

```
Query: 1   MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
           MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT
Sbjct: 1   MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
           TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
           FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLMLALL 240
           FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLMLALL
Sbjct: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLMLALL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
           ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI
Sbjct: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360
           LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS
Sbjct: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIIENRILKW 379
           LILILMPVAGIIENRILKW
Sbjct: 361 LILILMPVAGIIENRILKW 379
```

tr Q8HB83 Q8HB83_CAMDR **Cytochrome b [cytb] [Camelus dromedarius (Dromedary) (Arabian camel)]** 379 AA align

Score = 775 bits (2000), Expect = 0.0
Identities = 378/379 (99%), Positives = 379/379 (100%)

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Sbjct: 1   MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
           TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVG+VLL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGIVLL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
           FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLMLALL 240
           FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLMLALL
Sbjct: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLMLALL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
           ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI
Sbjct: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360
           LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS
Sbjct: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIIENRILKW 379
           LILILMPVAGIIENRILKW
Sbjct: 361 LILILMPVAGIIENRILKW 379
```

```
tr  Q8HBG5       Cytochrome b [cytb] [Camelus dromedarius (Dromedary) (Arabian  379 AA
    Q8HBG5_CAMDR camel)]                                                       align

 Score =  773 bits (1995), Expect = 0.0
 Identities = 377/379 (99%), Positives = 378/379 (99%)

Query: 1   MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
           MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT
Sbjct: 1   MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
           TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVG+VLL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGIVLL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
           FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLMLALL 240
           FHFILPFIITALVAVHLLFLHETGSNNPTGI SDMDKIPFHPYYTIKDILGALLLMLALL
Sbjct: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGIPSDMDKIPFHPYYTIKDILGALLLMLALL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
           ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI
Sbjct: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360
           LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS
Sbjct: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIIENRILKW 379
           LILILMPVAGIIENRILKW
Sbjct: 361 LILILMPVAGIIENRILKW 379



sp  Q34028     Cytochrome b [MT-CYB] [Camelus bactrianus (Bactrian camel)]  379 AA
    CYB_CAMBA                                                              align

 Score =  763 bits (1970), Expect = 0.0
 Identities = 371/379 (97%), Positives = 374/379 (98%)

Query: 1   MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
           MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT
Sbjct: 1   MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
           TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTF ETWNVG++LL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFLETWNVGIILL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
           FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLMLALL 240
           FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLML LL
Sbjct: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLMLILL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
           ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLAL+LSILI
Sbjct: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALILSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360
           LA IP LHTSKQRSM FRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS
Sbjct: 301 LALIPMLHTSKQRSMMFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIIENRILKW 379
           LILILMPVAGIIENRILKW
Sbjct: 361 LILILMPVAGIIENRILKW 379



tr  Q540T9       Cytochrome b [cytb] [Camelus bactrianus (Bactrian camel)]  379 AA
    Q540T9_CAMBA                                                           align

 Score =  763 bits (1970), Expect = 0.0
 Identities = 371/379 (97%), Positives = 374/379 (98%)

Query: 1   MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
           MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT
Sbjct: 1   MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
```

```
Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
           TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTF ETWNVG++LL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFLETWNVGIILL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
           FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLMLALL 240
           FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLML LL
Sbjct: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLMLILL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
           ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLAL+LSILI
Sbjct: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALILSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360
           LA IP LHTSKQRSM FRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS
Sbjct: 301 LALIPMLHTSKQRSMMFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIIENRILKW 379
           LILILMPVAGIIENRILKW
Sbjct: 361 LILILMPVAGIIENRILKW 379
```

tr Q8HFA8 Cytochrome b [cytb] [Camelus bactrianus (Bactrian camel)] 379 AA
Q8HFA8_CAMBA align

Score = 759 bits (1959), Expect = 0.0
Identities = 369/379 (97%), Positives = 372/379 (98%)

```
Query: 1   MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
           MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLI QILTGLFLAMHYTSDTT
Sbjct: 1   MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLITQILTGLFLAMHYTSDTT 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
           TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTF ETWNVG++LL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFLETWNVGIILL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
           FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLMLALL 240
           FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLML LL
Sbjct: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLMLILL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
           ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLAL+LSILI
Sbjct: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALILSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360
           LA IP LHTSKQRSM FRPISQCLFWVLVADLL LTWIGGQPVEPPFIMIGQVASILYFS
Sbjct: 301 LALIPMLHTSKQRSMMFRPISQCLFWVLVADLLALTWIGGQPVEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIIENRILKW 379
           LILILMPVAGIIENRILKW
Sbjct: 361 LILILMPVAGIIENRILKW 379
```

tr Q8HBR1 Cytochrome b [cytb] [Camelus bactrianus (Bactrian camel)] 379 AA
Q8HBR1_CAMBA align

Score = 754 bits (1948), Expect = 0.0
Identities = 365/379 (96%), Positives = 372/379 (98%)

```
Query: 1   MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
           MTN RKSHPLLKI+NDAFIDLPAPSNISSWWNFGSLLG+CLIMQILTGLFLAMHYTSDTT
Sbjct: 1   MTNTRKSHPLLKIVNDAFIDLPAPSNISSWWNFGSLLGICLIMQILTGLFLAMHYTSDTT 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
           TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTF ETWNVG++LL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFLETWNVGIILL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
           FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLMLALL 240
           FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLL+L LL
Sbjct: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLVLILL 240
```

```
Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
           ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLAL+LSILI
Sbjct: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALILSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360
           LA IP LHTSKQRSM FRPISQCLFWVLVADLLTLTWIGGQPVEPPFI+IGQ ASILYFS
Sbjct: 301 LALIPMLHTSKQRSMMFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIVIGQAASILYFS 360

Query: 361 LILILMPVAGIIENRILKW 379
           LILILMPVAGIIENRILKW
Sbjct: 361 LILILMPVAGIIENRILKW 379
```

tr Q8HFA7 Cytochrome b [cytb] [Camelus bactrianus (Bactrian camel)] 379 AA
Q8HFA7_CAMBA align

```
 Score =  753 bits (1944), Expect = 0.0
 Identities = 364/379 (96%), Positives = 371/379 (97%)

Query: 1   MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
           MTN RKSHPLLKI+NDAFIDLP PSNISSWWNFGSLLG+CLIMQILTGLFLAMHYTSDTT
Sbjct: 1   MTNTRKSHPLLKIVNDAFIDLPTPSNISSWWNFGSLLGICLIMQILTGLFLAMHYTSDTT 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
           TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTF ETWNVG++LL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFLETWNVGIILL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
           FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLMLALL 240
           FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLL+L LL
Sbjct: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLVLILL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
           ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLAL+LSILI
Sbjct: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALILSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360
           LA IP LHTSKQRSM FRPISQCLFWVLVADLLTLTWIGGQPVEPPFI+IGQ ASILYFS
Sbjct: 301 LALIPMLHTSKQRSMMFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIVIGQAASILYFS 360

Query: 361 LILILMPVAGIIENRILKW 379
           LILILMPVAGIIENRILKW
Sbjct: 361 LILILMPVAGIIENRILKW 379
```

tr Q5GH08 Cytochrome b [cytb] [Lama glama argentina] 379 AA
Q5GH08_LAMPA align

```
 Score =  747 bits (1929), Expect = 0.0
 Identities = 358/379 (94%), Positives = 369/379 (97%)

Query: 1   MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
           MTNIRKSHPLLKI+N+AFIDLPAPSNISSWWNFGSLLG+CLIMQI+TGLFLAMHYTSDTT
Sbjct: 1   MTNIRKSHPLLKIVNNAFIDLPAPSNISSWWNFGSLLGICLIMQIMTGLFLAMHYTSDTT 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
           TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSY F ETWN+G++LL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYAFLETWNIGIILL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
           FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPY+GTTLVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYVGTTLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLMLALL 240
           FHFILPFII AL  VHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLL+L LL
Sbjct: 181 FHFILPFIIAALAGVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLILILL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
           +LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLAL+LSILI
Sbjct: 241 LLVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALILSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360
           LAFIP LHTSKQRSM FRPISQCLFW LVADLLTLTWIGGQPVEPPFIMIGQVASILYFS
Sbjct: 301 LAFIPLLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIIENRILKW 379
           LILILMPVAGIIEN ILKW
```

```
Sbjct: 361 LILILMPVAGIIENHILKW 379
```

sp Q36227 **Cytochrome b [MT-CYB] [Lama vicugna (Vicugna) (Vicugna vicugna)]** 379 AA
CYB_LAMVI align

```
 Score =  745 bits (1924), Expect = 0.0
 Identities = 357/379 (94%), Positives = 368/379 (97%)

Query: 1   MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
           MTNIRKSHPLLKI+N+AFIDLPAPSNISSWWNFGSLLG+CLIMQI+TGLFLAMHYTSDTT
Sbjct: 1   MTNIRKSHPLLKIVNNAFIDLPAPSNISSWWNFGSLLGICLIMQIMTGLFLAMHYTSDTT 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
           TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSY F ETWN+G++LL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYAFLETWNIGIILL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
           FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPY+GTTLVEWIWGGFSVDKATL RFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYVGTTLVEWIWGGFSVDKATLNRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLMLALL 240
           FHFILPFII AL  VHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLL+L LL
Sbjct: 181 FHFILPFIIAALAGVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLILILL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
           +LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLAL+LSILI
Sbjct: 241 LLVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALILSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360
           LAFIP LHTSKQRSM FRPISQCLFW LVADLLTLTWIGGQPVEPPFIMIGQVASILYFS
Sbjct: 301 LAFIPLLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIIENRILKW 379
           LILILMPVAGIIEN ILKW
Sbjct: 361 LILILMPVAGIIENHILKW 379
```

sp Q34891 **Cytochrome b [MT-CYB] [Lama glama (Llama)]** 379 AA
CYB_LAMGL align

```
 Score =  745 bits (1924), Expect = 0.0
 Identities = 357/379 (94%), Positives = 368/379 (97%)

Query: 1   MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
           MTNIRKSHPLLKI+N+AFIDLPAPSNISSWWNFGSLLG+CLIMQI+TGLFLAMHYTSDTT
Sbjct: 1   MTNIRKSHPLLKIVNNAFIDLPAPSNISSWWNFGSLLGICLIMQIMTGLFLAMHYTSDTT 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
           TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSY F ETWN+G++LL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYAFLETWNIGIILL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
           FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPY+GTTLVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYVGTTLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLMLALL 240
           FHFILPF+I AL  VHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLL+L LL
Sbjct: 181 FHFILPFVIAALAGVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLILTLL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
           +LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI
Sbjct: 241 LLVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360
           LA IP LHTSKQRSM FRPISQCLFW LVADLLTLTWIGGQPVEPPFIMIGQVASILYFS
Sbjct: 301 LALIPLLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIIENRILKW 379
           LILILMPVAGIIEN ILKW
Sbjct: 361 LILILMPVAGIIENHILKW 379
```

tr Q5GH03 **Cytochrome b [cytb] [Lama guanicoe huanacus]** 379 AA
Q5GH03_LAMGU align

```
 Score =  745 bits (1924), Expect = 0.0
 Identities = 357/379 (94%), Positives = 368/379 (97%)

Query: 1   MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
           MTNIRKSHPLLKI+N+AFIDLPAPSNISSWWNFGSLLG+CLIMQI+TGLFLAMHYTSDTT
Sbjct: 1   MTNIRKSHPLLKIVNNAFIDLPAPSNISSWWNFGSLLGICLIMQIMTGLFLAMHYTSDTT 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
           TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSY F ETWN+G++LL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYAFLETWNIGIILL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
           FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPY+GTTLVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYVGTTLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLMLALL 240
           FHFILPF+I AL  VHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLL+L LL
Sbjct: 181 FHFILPFVIAALAGVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLILTLL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
           +LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI
Sbjct: 241 LLVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360
           LA IP LHTSKQRSM FRPISQCLFW LVADLLTLTWIGGQPVEPPFIMIGQVASILYFS
Sbjct: 301 LALIPLLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIIENRILKW 379
           LILILMPVAGIIEN ILKW
Sbjct: 361 LILILMPVAGIIENHILKW 379
```

tr Q5GH04 **Cytochrome b [cytb] [Lama guanicoe cacsilensis]** 379 AA
Q5GH04_LAMGU align

```
 Score =  745 bits (1924), Expect = 0.0
 Identities = 357/379 (94%), Positives = 368/379 (97%)

Query: 1   MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
           MTNIRKSHPLLKI+N+AFIDLPAPSNISSWWNFGSLLG+CLIMQI+TGLFLAMHYTSDTT
Sbjct: 1   MTNIRKSHPLLKIVNNAFIDLPAPSNISSWWNFGSLLGICLIMQIMTGLFLAMHYTSDTT 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
           TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSY F ETWN+G++LL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYAFLETWNIGIILL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
           FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPY+GTTLVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYVGTTLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLMLALL 240
           FHFILPF+I AL  VHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLL+L LL
Sbjct: 181 FHFILPFVIAALAGVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLILTLL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
           +LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI
Sbjct: 241 LLVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360
           LA IP LHTSKQRSM FRPISQCLFW LVADLLTLTWIGGQPVEPPFIMIGQVASILYFS
Sbjct: 301 LALIPLLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIIENRILKW 379
           LILILMPVAGIIEN ILKW
Sbjct: 361 LILILMPVAGIIENHILKW 379
```

tr Q70LJ9 **Cytochrome b [cytb] [Lama guanicoe pacos (Alpaca) (Lama pacos)]** 379 AA
Q70LJ9_LAMPA align

```
 Score =  745 bits (1924), Expect = 0.0
 Identities = 357/379 (94%), Positives = 368/379 (97%)

Query: 1   MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
           MTNIRKSHPLLKI+N+AFIDLPAPSNISSWWNFGSLLG+CLIMQI+TGLFLAMHYTSDTT
Sbjct: 1   MTNIRKSHPLLKIVNNAFIDLPAPSNISSWWNFGSLLGICLIMQIMTGLFLAMHYTSDTT 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
           TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSY F ETWN+G++LL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYAFLETWNIGIILL 120
```

```
Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
           FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPY+GTTLVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYVGTTLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLMLALL 240
           FHFILPF+I AL  VHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLL+L LL
Sbjct: 181 FHFILPFVIAALAGVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLILTLL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
           +LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI
Sbjct: 241 LLVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360
           LA IP LHTSKQRSM FRPISQCLFW LVADLLTLTWIGGQPVEPPFIMIGQVASILYFS
Sbjct: 301 LALIPLLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIIENRILKW 379
           LILILMPVAGIIEN ILKW
Sbjct: 361 LILILMPVAGIIENHILKW 379
```

sp Q34916 Cytochrome b [MT-CYB] [Lama guanicoe pacos (Alpaca) (Lama pacos)] 379 AA
CYB_LAMPA align

```
 Score =  744 bits (1920), Expect = 0.0
 Identities = 357/379 (94%), Positives = 368/379 (97%)

Query: 1   MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
           MTNIRKSHPLLKI+N+AFIDLPAPSNISSWWNFGSLLG+CLIMQI+TGLFLAMHYTSDTT
Sbjct: 1   MTNIRKSHPLLKIVNNAFIDLPAPSNISSWWNFGSLLGICLIMQIMTGLFLAMHYTSDTT 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
           TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSY F ETWN+G++LL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYAFLETWNIGIILL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
           FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPY+GTTLVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYVGTTLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLMLALL 240
           FHFILPFII AL  VHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLL+L LL
Sbjct: 181 FHFILPFIIAALAGVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLILILL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
           +LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLAL+LSILI
Sbjct: 241 LLVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALILSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360
           LAFIP LHTSKQRSM FRPISQCLFW LVADLLTLTWIGGQPVEPPFIMIGQVASIL FS
Sbjct: 301 LAFIPLLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQPVEPPFIMIGQVASILSFS 360

Query: 361 LILILMPVAGIIENRILKW 379
           LILILMPVAGIIEN ILKW
Sbjct: 361 LILILMPVAGIIENHILKW 379
```

tr Q5GH09 Cytochrome b [cytb] [Lama glama chaku] 379 AA
Q5GH09_LAMPA align

```
 Score =  744 bits (1920), Expect = 0.0
 Identities = 356/379 (93%), Positives = 367/379 (96%)

Query: 1   MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
           MTNIRKSHPLLKI+N+AFIDLPAPSNISSWWNFGSLLG+CLIMQI+TGLFLAMHYTSDTT
Sbjct: 1   MTNIRKSHPLLKIVNNAFIDLPAPSNISSWWNFGSLLGICLIMQIMTGLFLAMHYTSDTT 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
           TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSY F ETWN+G++LL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYAFLETWNIGIILL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
           FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPY+GTTLVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYVGTTLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLMLALL 240
           FHFILPF+I AL  VHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILG LLL+L LL
Sbjct: 181 FHFILPFVIAALAGVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGVLLLILTLL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
           +LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI
```

```
Sbjct: 241 LLVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360
           LA IP LHTSKQRSM FRPISQCLFW LVADLLTLTWIGGQPVEPPFIMIGQVASILYFS
Sbjct: 301 LALIPLLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIIENRILKW 379
           LILILMPVAGIIEN ILKW
Sbjct: 361 LILILMPVAGIIENHILKW 379
```

```
tr  Q5GH11          Cytochrome b [cytb] [Lama pacos suri]          379 AA
    Q5GH11_LAMPA                                                  align

 Score =  744 bits (1920), Expect = 0.0
 Identities = 356/379 (93%), Positives = 367/379 (96%)

Query: 1   MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
           MTNIRKSHPLLKI+N+AFIDLPAPSNISSWWNFGSLLG+CLIMQI+TGLFLAMHYTSDTT
Sbjct: 1   MTNIRKSHPLLKIVNNAFIDLPAPSNISSWWNFGSLLGICLIMQIMTGLFLAMHYTSDTT 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
           TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSY F ETWN+G++LL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYAFLETWNIGIILL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
           FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPY+GTTLVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYVGTTLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLMLALL 240
           FHFILPF+I AL  VHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILG LLL+L LL
Sbjct: 181 FHFILPFVIAALAGVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGVLLLILTLL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
           +LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI
Sbjct: 241 LLVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360
           LA IP LHTSKQRSM FRPISQCLFW LVADLLTLTWIGGQPVEPPFIMIGQVASILYFS
Sbjct: 301 LALIPLLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIIENRILKW 379
           LILILMPVAGIIEN ILKW
Sbjct: 361 LILILMPVAGIIENHILKW 379
```

```
tr  Q5GH06          Cytochrome b [cytb] [Lama guanicoe cacsilensis]   379 AA
    Q5GH06_LAMGU                                                     align

 Score =  743 bits (1917), Expect = 0.0
 Identities = 355/379 (93%), Positives = 367/379 (96%)

Query: 1   MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
           MTNIRKSHPLLKI+N+A+IDLPAPSNISSWWNFGSLLG+CLIMQI+TGLFLAMHYTSDTT
Sbjct: 1   MTNIRKSHPLLKIVNNAYIDLPAPSNISSWWNFGSLLGICLIMQIMTGLFLAMHYTSDTT 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
           TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSY F ETWN+G++LL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYAFLETWNIGIILL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
           FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPY+GTTLVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYVGTTLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLMLALL 240
           FHFILPF+I AL  VHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILG LLL+L LL
Sbjct: 181 FHFILPFVIAALAGVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGVLLLILTLL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
           +LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI
Sbjct: 241 LLVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360
           LA IP LHTSKQRSM FRPISQCLFW LVADLLTLTWIGGQPVEPPFIMIGQVASILYFS
Sbjct: 301 LALIPLLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIIENRILKW 379
           LILILMPVAGIIEN ILKW
Sbjct: 361 LILILMPVAGIIENHILKW 379
```

```
sp  Q34890      Cytochrome b [MT-CYB] [Lama guanicoe (Guanaco)]      379 AA
    CYB_LAMGU                                                       align

 Score =  742 bits (1915), Expect = 0.0
 Identities = 355/379 (93%), Positives = 366/379 (96%)

Query: 1   MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
           MTNIRKSHPLLKI+N+AFIDLPAPSNISSWWNFGSLLG+CLIMQI+TGLFLAMHYTSDT
Sbjct: 1   MTNIRKSHPLLKIVNNAFIDLPAPSNISSWWNFGSLLGICLIMQIMTGLFLAMHYTSDTA 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
           TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSY F ETWN+G++LL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYAFLETWNIGIILL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
           FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPY+GTTLVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYVGTTLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLMLALL 240
           FHFILPF+I AL  VHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILG LLL+L LL
Sbjct: 181 FHFILPFVIAALAGVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGVLLLILTLL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
           +LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI
Sbjct: 241 LLVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360
           LA IP LHTSKQRSM FRPISQCLFW LVADLLTLTWIGGQPVEPPFIMIGQVASILYFS
Sbjct: 301 LALIPLLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIIENRILKW 379
           LILILMPVAGIIEN ILKW
Sbjct: 361 LILILMPVAGIIENHILKW 379
```

```
tr  Q5GH02      Cytochrome b [cytb] [Lama guanicoe huanacus]      379 AA
    Q5GH02_LAMGU                                                 align

 Score =  742 bits (1915), Expect = 0.0
 Identities = 355/379 (93%), Positives = 366/379 (96%)

Query: 1   MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
           MTNIRKSHPLLKI+N+AFIDLPAPSNISSWWNFGSLLG+CLIMQI+TGLFLAMHYTSDT
Sbjct: 1   MTNIRKSHPLLKIVNNAFIDLPAPSNISSWWNFGSLLGICLIMQIMTGLFLAMHYTSDTA 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
           TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSY F ETWN+G++LL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYAFLETWNIGIILL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
           FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPY+GTTLVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYVGTTLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLMLALL 240
           FHFILPF+I AL  VHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILG LLL+L LL
Sbjct: 181 FHFILPFVIAALAGVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGVLLLILTLL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
           +LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI
Sbjct: 241 LLVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360
           LA IP LHTSKQRSM FRPISQCLFW LVADLLTLTWIGGQPVEPPFIMIGQVASILYFS
Sbjct: 301 LALIPLLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIIENRILKW 379
           LILILMPVAGIIEN ILKW
Sbjct: 361 LILILMPVAGIIENHILKW 379
```

```
tr  Q5GGY6      Cytochrome b [cytb] [Lama guanicoe guanicoe]      379 AA
    Q5GGY6_LAMGU                                                 align

 Score =  742 bits (1915), Expect = 0.0
 Identities = 355/379 (93%), Positives = 366/379 (96%)

Query: 1   MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
           MTNIRKSHPLLKI+N+AFIDLPAPSNISSWWNFGSLLG+CLIMQI+TGLFLAMHYTSDT
Sbjct: 1   MTNIRKSHPLLKIVNNAFIDLPAPSNISSWWNFGSLLGICLIMQIMTGLFLAMHYTSDTA 60
```

```
Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
           TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSY F ETWN+G++LL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYAFLETWNIGIILL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
           FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPY+GTTLVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYVGTTLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLMLALL 240
           FHFILPF+I AL  VHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILG LLL+L LL
Sbjct: 181 FHFILPFVIAALAGVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGVLLLILTLL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
           +LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI
Sbjct: 241 LLVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360
           LA IP LHTSKQRSM FRPISQCLFW LVADLLTLTWIGGQPVEPPFIMIGQVASILYFS
Sbjct: 301 LALIPLLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIIENRILKW 379
           LILILMPVAGIIEN ILKW
Sbjct: 361 LILILMPVAGIIENHILKW 379
```

tr Q5GH05 **Cytochrome b [cytb] [Lama guanicoe cacsilensis]** 379 AA
Q5GH05_LAMGU align

```
 Score =  742 bits (1915), Expect = 0.0
 Identities = 355/379 (93%), Positives = 366/379 (96%)

Query: 1   MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
           MTNIRKSHPLLKI+N+AFIDLPAPSNISSWWNFGSLLG+CLIMQI+TGLFLAMHYTSDT
Sbjct: 1   MTNIRKSHPLLKIVNNAFIDLPAPSNISSWWNFGSLLGICLIMQIMTGLFLAMHYTSDTA 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
           TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSY F ETWN+G++LL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYAFLETWNIGIILL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
           FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPY+GTTLVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYVGTTLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLMLALL 240
           FHFILPF+I AL  VHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILG LLL+L LL
Sbjct: 181 FHFILPFVIAALAGVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGVLLLILTLL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
           +LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI
Sbjct: 241 LLVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360
           LA IP LHTSKQRSM FRPISQCLFW LVADLLTLTWIGGQPVEPPFIMIGQVASILYFS
Sbjct: 301 LALIPLLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIIENRILKW 379
           LILILMPVAGIIEN ILKW
Sbjct: 361 LILILMPVAGIIENHILKW 379
```

tr Q5GGY0 **Cytochrome b [cytb] [Lama guanicoe guanicoe]** 379 AA
Q5GGY0_LAMGU align

```
 Score =  741 bits (1914), Expect = 0.0
 Identities = 355/379 (93%), Positives = 366/379 (96%)

Query: 1   MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
           MTNIRKSHPLLKI+N+AFIDLPAPSNISSWWNFGSLLG+CLIMQI+TGLFLAMHYTSDT
Sbjct: 1   MTNIRKSHPLLKIVNNAFIDLPAPSNISSWWNFGSLLGICLIMQIMTGLFLAMHYTSDTA 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
           TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSY F ETWN+G++LL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYAFLETWNIGIILL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
           FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPY+GTTLVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYLGTTLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLMLALL 240
           FHFILPF+I AL  VHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILG LLL+L LL
```

```
Sbjct: 181 FHFILPFVIAALAGVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGVLLLILTLL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
           +LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI
Sbjct: 241 LLVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360
           LA IP LHTSKQRSM FRPISQCLFW LVADLLTLTWIGGQPVEPPFIMIGQVASILYFS
Sbjct: 301 LALIPLLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIIENRILKW 379
           LILILMPVAGIIEN ILKW
Sbjct: 361 LILILMPVAGIIENHILKW 379
```

tr O03364 Cytochrome b [Lama guanicoe (Guanaco)] 379 AA
O03364_LAMGU align

Score = 741 bits (1913), Expect = 0.0
Identities = 355/379 (93%), Positives = 366/379 (96%)

```
Query: 1   MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
           MTNIRKSHPLLKI+N+AFIDLPAPSNISSWWNFGSLLG+CLIMQI+TGLFLAMHYTSDT
Sbjct: 1   MTNIRKSHPLLKIVNNAFIDLPAPSNISSWWNFGSLLGICLIMQIMTGLFLAMHYTSDTA 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
           TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSY F ETWN+G++LL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYAFLETWNIGIILL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
           FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPY+GTTLVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYVGTTLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLMLALL 240
           FHFILPF+I AL  VHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILG LLL+L LL
Sbjct: 181 FHFILPFVIAALAGVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGVLLLILTLL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
           +LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI
Sbjct: 241 LLVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360
           LA IP LHTSKQRSM FRPISQCLFW LVADLLTLTWIGGQPVEPPFIMIGQVASILYFS
Sbjct: 301 LALIPLLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIIENRILKW 379
           LILILMPVAGIIEN ILKW
Sbjct: 361 LILILMPVAGIIENYILKW 379
```

tr Q5GGZ3 Cytochrome b [cytb] [Lama guanicoe huanacus] 379 AA
Q5GGZ3_LAMGU align

Score = 741 bits (1912), Expect = 0.0
Identities = 355/379 (93%), Positives = 366/379 (96%)

```
Query: 1   MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
           MTNIRKSHPLLKI+N+AFIDLPAPSNISSWWNFGSLLG+CLIMQI+TGLFLAMHYTSDTT
Sbjct: 1   MTNIRKSHPLLKIVNNAFIDLPAPSNISSWWNFGSLLGICLIMQIMTGLFLAMHYTSDTT 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
           TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSY F ETWN+G++LL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYAFLETWNIGIILL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
           FTVMATAFMGYVLPWGQMSFWGA VITNLLSAIPY+GT LVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGAPVITNLLSAIPYVGTPLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLMLALL 240
           FHFILPF+I AL  VHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLL+L LL
Sbjct: 181 FHFILPFVIAALAGVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLILTLL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
           +LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI
Sbjct: 241 LLVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360
           LA IP LHTSKQRSM FRPISQCLFW LVADLLTLTWIGGQPVEPPFIMIGQVASILYFS
Sbjct: 301 LALIPLLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIIENRILKW 379
```

```
          LILILMPVAGIIEN ILKW
Sbjct: 361 LILILMPVAGIIENHILKW 379
```

tr Q5GGY2 Cytochrome b [cytb] [Lama guanicoe guanicoe] 379 AA
Q5GGY2_LAMGU align

```
 Score =  741 bits (1912), Expect = 0.0
 Identities = 354/379 (93%), Positives = 366/379 (96%)

Query: 1   MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
           MTNIRKSHPLLKI+N+AFIDLPAPSNISSWWNFGSLLG+CLIMQI+TGLFLAMHYTSDT
Sbjct: 1   MTNIRKSHPLLKIVNNAFIDLPAPSNISSWWNFGSLLGICLIMQIMTGLFLAMHYTSDTA 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
           TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSY F ETWN+G++LL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYAFLETWNIGIILL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
           FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPY+GTTLVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYVGTTLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLMLALL 240
           FHFILPF+I AL  VHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILG LLL+L LL
Sbjct: 181 FHFILPFVIAALAGVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGVLLLILTLL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
           +LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI
Sbjct: 241 LLVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360
           LA IP LHTSKQRSM FRPISQCLFW LVADLLTLTWIGGQPVEPPFIM+GQVASILYFS
Sbjct: 301 LALIPLLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQPVEPPFIMMGQVASILYFS 360

Query: 361 LILILMPVAGIIENRILKW 379
           LILILMPVAGIIEN ILKW
Sbjct: 361 LILILMPVAGIIENHILKW 379
```

tr Q5GGZ7 Cytochrome b [cytb] [Lama guanicoe huanacus] 379 AA
Q5GGZ7_LAMGU align

```
 Score =  740 bits (1911), Expect = 0.0
 Identities = 354/379 (93%), Positives = 365/379 (96%)

Query: 1   MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
           MTNIRKSHPLLKI+N+AFIDLP PSNISSWWNFGSLLG+CLIMQI+TGLFLAMHYTSDT
Sbjct: 1   MTNIRKSHPLLKIVNNAFIDLPTPSNISSWWNFGSLLGICLIMQIMTGLFLAMHYTSDTA 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
           TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSY F ETWN+G++LL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYAFLETWNIGIILL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
           FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPY+GTTLVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYVGTTLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLMLALL 240
           FHFILPF+I AL  VHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILG LLL+L LL
Sbjct: 181 FHFILPFVIAALAGVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGVLLLILTLL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
           +LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI
Sbjct: 241 LLVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360
           LA IP LHTSKQRSM FRPISQCLFW LVADLLTLTWIGGQPVEPPFIMIGQVASILYFS
Sbjct: 301 LALIPLLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIIENRILKW 379
           LILILMPVAGIIEN ILKW
Sbjct: 361 LILILMPVAGIIENHILKW 379
```

tr Q5GH07 Cytochrome b [cytb] [Vicugna vicugna mensalis] 379 AA
Q5GH07_LAMVI align

```
 Score =  739 bits (1908), Expect = 0.0
 Identities = 355/379 (93%), Positives = 366/379 (96%)

Query: 1   MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
           MTN RKSHP LKI+N+AFIDLPAPSNISSWWNFGSLLG+CLIMQI+TGLFLAMHYTSDTT
Sbjct: 1   MTNYRKSHPPLKIVNNAFIDLPAPSNISSWWNFGSLLGICLIMQIMTGLFLAMHYTSDTT 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
           TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYI VGRGLYYGSY F ETWN+G++LL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIFVGRGLYYGSYAFLETWNIGIILL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
           FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPY+GTTLVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYVGTTLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLMLALL 240
           FHFILPFII AL  VHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLL+L LL
Sbjct: 181 FHFILPFIIAALAGVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLILILL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
           +LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLAL+LSILI
Sbjct: 241 LLVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALILSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360
           LAFIP LHTSKQRSM FRPISQCLFW LVADLLTLTWIGGQPVEPPFIMIGQVASILYFS
Sbjct: 301 LAFIPLLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIIENRILKW 379
           LILILMPVAGIIEN ILKW
Sbjct: 361 LILILMPVAGIIENHILKW 379
```

tr Q5GGY8 **Cytochrome b [cytb] [Lama guanicoe huanacus]** 379 AA
Q5GGY8_LAMGU align

```
 Score =  739 bits (1907), Expect = 0.0
 Identities = 354/379 (93%), Positives = 365/379 (96%)

Query: 1   MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
           MTNIRKSHPLLKI+N+AFIDLPAPSNISSWWNFGSLLG+CLIMQI+TGLFLAMHYTSDT
Sbjct: 1   MTNIRKSHPLLKIVNNAFIDLPAPSNISSWWNFGSLLGICLIMQIMTGLFLAMHYTSDTA 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
           TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSY F ETWN+G++LL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYAFLETWNIGIILL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
           FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPY+GTTLVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYVGTTLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLMLALL 240
           FHFILPF+I AL  VHLLFLHETGSNNPTGISSDM KIPFHPYYTIKDILG LLL+L LL
Sbjct: 181 FHFILPFVIAALAGVHLLFLHETGSNNPTGISSDMAKIPFHPYYTIKDILGVLLLILTLL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
           +LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI
Sbjct: 241 LLVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360
           LA IP LHTSKQRSM FRPISQCLFW LVADLLTLTWIGGQPVEPPFIMIGQVASILYFS
Sbjct: 301 LALIPLLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360

Query: 361 LILILMPVAGIIENRILKW 379
           LILILMPVAGIIEN ILKW
Sbjct: 361 LILILMPVAGIIENHILKW 379
```

tr Q5GGY9 **Cytochrome b [cytb] [Lama guanicoe huanacus]** 379 AA
Q5GGY9_LAMGU align

```
 Score =  738 bits (1904), Expect = 0.0
 Identities = 353/379 (93%), Positives = 364/379 (96%)

Query: 1   MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
           MTNIRKSHPLLKI+N+AFIDLPAPSNISSWWNFGSLLG+CLIMQI+TGLFLAMHYTSDT
Sbjct: 1   MTNIRKSHPLLKIVNNAFIDLPAPSNISSWWNFGSLLGICLIMQIMTGLFLAMHYTSDTA 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
           TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSY F ETWN+G++LL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYAFLETWNIGIILL 120
```

```
Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
           FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPY+GTTLVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYVGTTLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLMLALL 240
           FHFILPF+I AL  VHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILG LLL+L LL
Sbjct: 181 FHFILPFVIAALAGVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGVLLLILTLL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
           +LVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI
Sbjct: 241 LLVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360
           L  IP LHTSKQRSM FRPISQCLFW LVADLLTLTWIGGQPVEPPFIMIGQVASILY S
Sbjct: 301 LPLIPLLHTSKQRSMMFRPISQCLFWTLVADLLTLTWIGGQPVEPPFIMIGQVASILYLS 360

Query: 361 LILILMPVAGIIENRILKW 379
           LILILMPVAGIIEN ILKW
Sbjct: 361 LILILMPVAGIIENHILKW 379
```

sp Q5BQG9 **Cytochrome b [MT-CYB] [Sus philippensis (Philippine warty pig)]** 379 AA
CYB_SUSPH align

Score = 723 bits (1866), Expect = 0.0
Identities = 343/379 (90%), Positives = 363/379 (95%)

```
Query: 1   MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
           MTNIRKSHPL+KI+N+AFIDLPAPSNISSWWNFGSLLG+CLI+QILTGLFLAMHYTSDTT
Sbjct: 1   MTNIRKSHPLMKIINNAFIDLPAPSNISSWWNFGSLLGICLILQILTGLFLAMHYTSDTT 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
           TAFSSVAHICRDVNYGWIIRYLHANGASMFFICL+IHVGRGLYYGSY F ETWN+G++LL
Sbjct: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLFIHVGRGLYYGSYMFLETWNIGVILL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
           FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGT LVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTDLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLMLALL 240
           FHFILPFIITAL AVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGAL +ML LL
Sbjct: 181 FHFILPFIITALAAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALFMMLILL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
           ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALV SILI
Sbjct: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVASILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360
           L  +P LHTSKQRSM FRP+SQCLFW+LVADL+TLTWIGGQPVE PFI+IGQ+ASILYF
Sbjct: 301 LILMPMLHTSKQRSMMFRPLSQCLFWMLVADLITLTWIGGQPVEHPFIIIGQLASILYFL 360

Query: 361 LILILMPVAGIIENRILKW 379
           +IL+LMP+  IIEN +LKW
Sbjct: 361 IILVLMPITSIIENNLLKW 379
```

tr Q9TGH5 **Cytochrome b [cytb] [Tragelaphus strepsiceros (Greater kudu)]** 379 AA
Q9TGH5_TRAST align

Score = 723 bits (1866), Expect = 0.0
Identities = 339/379 (89%), Positives = 365/379 (96%)

```
Query: 1   MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
           MTNIRKSHPL+KI+N+AFIDLPAPSNISSWWNFGSLLG+CLI+QILTGLFLAMHYTSDTT
Sbjct: 1   MTNIRKSHPLMKIVNNAFIDLPAPSNISSWWNFGSLLGICLILQILTGLFLAMHYTSDTT 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
           TAFSSV HICRDVNYGWIIRY+HANGASMFFICLY+HVGRG+YYGSYTF ETWN+G++LL
Sbjct: 61  TAFSSVTHICRDVNYGWIIRYMHANGASMFFICLYVHVGRGMYYGSYTFLETWNIGVILL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
           FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGT LVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTNLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLMLALL 240
           FHFILPFII AL  VHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLL+LAL+
Sbjct: 181 FHFILPFIIAALAMVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLVLALM 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
           +LVLF+PDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI
```

```
Sbjct: 241 LLVLFTPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360
           L F+P LHTSKQRSM FRP+SQCLFW+LVADLLTLTWIGGQPVE P+++IGQ+ASI+YF
Sbjct: 301 LIFLPLLHTSKQRSMMFRPLSQCLFWILVADLLTLTWIGGQPVEHPYMIIGQLASIMYFL 360

Query: 361 LILILMPVAGIIENRILKW 379
           LIL+LMPV  +IEN +LKW
Sbjct: 361 LILVLMPVTSMIENNLLKW 379
```

tr Q5MG70 Cytochrome b [CYTB] [Sus scrofa coreanus] 379 AA
Q5MG70_PIG align

```
 Score =  722 bits (1863), Expect = 0.0
 Identities = 343/379 (90%), Positives = 362/379 (95%)

Query: 1   MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
           MTNIRKSHPL+KI+N+AFIDLPAPSNISSWWNFGSLLG+CLI+QILTGLFLAMHYTSDTT
Sbjct: 1   MTNIRKSHPLMKIINNAFIDLPAPSNISSWWNFGSLLGICLILQILTGLFLAMHYTSDTT 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
           TAFSSV HICRDVNYGWIIRYLHANGASMFFICL+IHVGRGLYYGSY F ETWN+G+VLL
Sbjct: 61  TAFSSVTHICRDVNYGWIIRYLHANGASMFFICLFIHVGRGLYYGSYMFLETWNIGVVLL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
           FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGT LVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTDLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLMLALL 240
           FHFILPFIITAL AVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGAL +ML LL
Sbjct: 181 FHFILPFIITALAAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALFMMLILL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
           ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALV SILI
Sbjct: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVASILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360
           L  +P LHTSKQRSM FRP+SQCLFW+LVADL+TLTWIGGQPVE PFI+IGQ+ASILYF
Sbjct: 301 LILMPMLHTSKQRSMMFRPLSQCLFWMLVADLITLTWIGGQPVEHPFIIIGQLASILYFL 360

Query: 361 LILILMPVAGIIENRILKW 379
           +IL+LMP+  IIEN +LKW
Sbjct: 361 IILVLMPITSIIENNLLKW 379
```

tr Q079P0 Cytochrome b [CYTB] [Sus scrofa (Pig)] 379 AA
Q079P0_PIG align

```
 Score =  722 bits (1863), Expect = 0.0
 Identities = 343/379 (90%), Positives = 362/379 (95%)

Query: 1   MTNIRKSHPLLKIMNDAFIDLPAPSNISSWWNFGSLLGVCLIMQILTGLFLAMHYTSDTT 60
           MTNIRKSHPL+KI+N+AFIDLPAPSNISSWWNFGSLLG+CLI+QILTGLFLAMHYTSDTT
Sbjct: 1   MTNIRKSHPLMKIINNAFIDLPAPSNISSWWNFGSLLGICLILQILTGLFLAMHYTSDTT 60

Query: 61  TAFSSVAHICRDVNYGWIIRYLHANGASMFFICLYIHVGRGLYYGSYTFSETWNVGMVLL 120
           TAFSSV HICRDVNYGWIIRYLHANGASMFFICL+IHVGRGLYYGSY F ETWN+G+VLL
Sbjct: 61  TAFSSVTHICRDVNYGWIIRYLHANGASMFFICLFIHVGRGLYYGSYMFLETWNIGVVLL 120

Query: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTTLVEWIWGGFSVDKATLTRFFA 180
           FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGT LVEWIWGGFSVDKATLTRFFA
Sbjct: 121 FTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTDLVEWIWGGFSVDKATLTRFFA 180

Query: 181 FHFILPFIITALVAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALLLMLALL 240
           FHFILPFIITAL AVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGAL +ML LL
Sbjct: 181 FHFILPFIITALAAVHLLFLHETGSNNPTGISSDMDKIPFHPYYTIKDILGALFMMLILL 240

Query: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVLSILI 300
           ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALV SILI
Sbjct: 241 ILVLFSPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALVASILI 300

Query: 301 LAFIPALHTSKQRSMTFRPISQCLFWVLVADLLTLTWIGGQPVEPPFIMIGQVASILYFS 360
           L  +P LHTSKQRSM FRP+SQCLFW+LVADL+TLTWIGGQPVE PFI+IGQ+ASILYF
Sbjct: 301 LILMPMLHTSKQRSMMFRPLSQCLFWMLVADLITLTWIGGQPVEHPFIIIGQLASILYFL 360

Query: 361 LILILMPVAGIIENRILKW 379
           +IL+LMP+  IIEN +LKW
Sbjct: 361 IILVLMPITSIIENNLLKW 379
```

Ex, H

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Welcome to the SIB BLAST Network Service

If results of this search are reported or published, please mention that
the computation was performed at the SIB using the BLAST network service.
The SIB BLAST network service uses a server developed at SIB and the NCBI
BLAST 2 software.

In case of problems, please read the online BLAST help.
If your question is not covered, please contact <helpdesk@expasy.org>.

NCBI BLAST program reference [PMID:9254694]:
Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W.,
Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein
database search programs. Nucleic Acids Res. 25:3389-3402(1997).

==========

Query: 141 AA
Date run: 2007-02-09 18:37:24 UTC+0100 on blast01.vital-it.ch
Program: NCBI BLASTP 2.2.15 [Oct-15-2006]
Database: UniProtKB Mammalia
240,475 sequences; 91,865,493 total letters
UniProt Knowledgebase Release 9.6 consists of:
UniProtKB/Swiss-Prot Release 51.6 of 06-Feb-2007: 257964 entries
UniProtKB/TrEMBL Release 34.6 of 06-Feb-2007: 3745801 entries

Taxonomic view | NiceBlast view | Printable view

List of potentially matching sequences

Send selected sequences to Clustal W (multiple alignment) Submit Query Select up to...

☐ Include query sequence

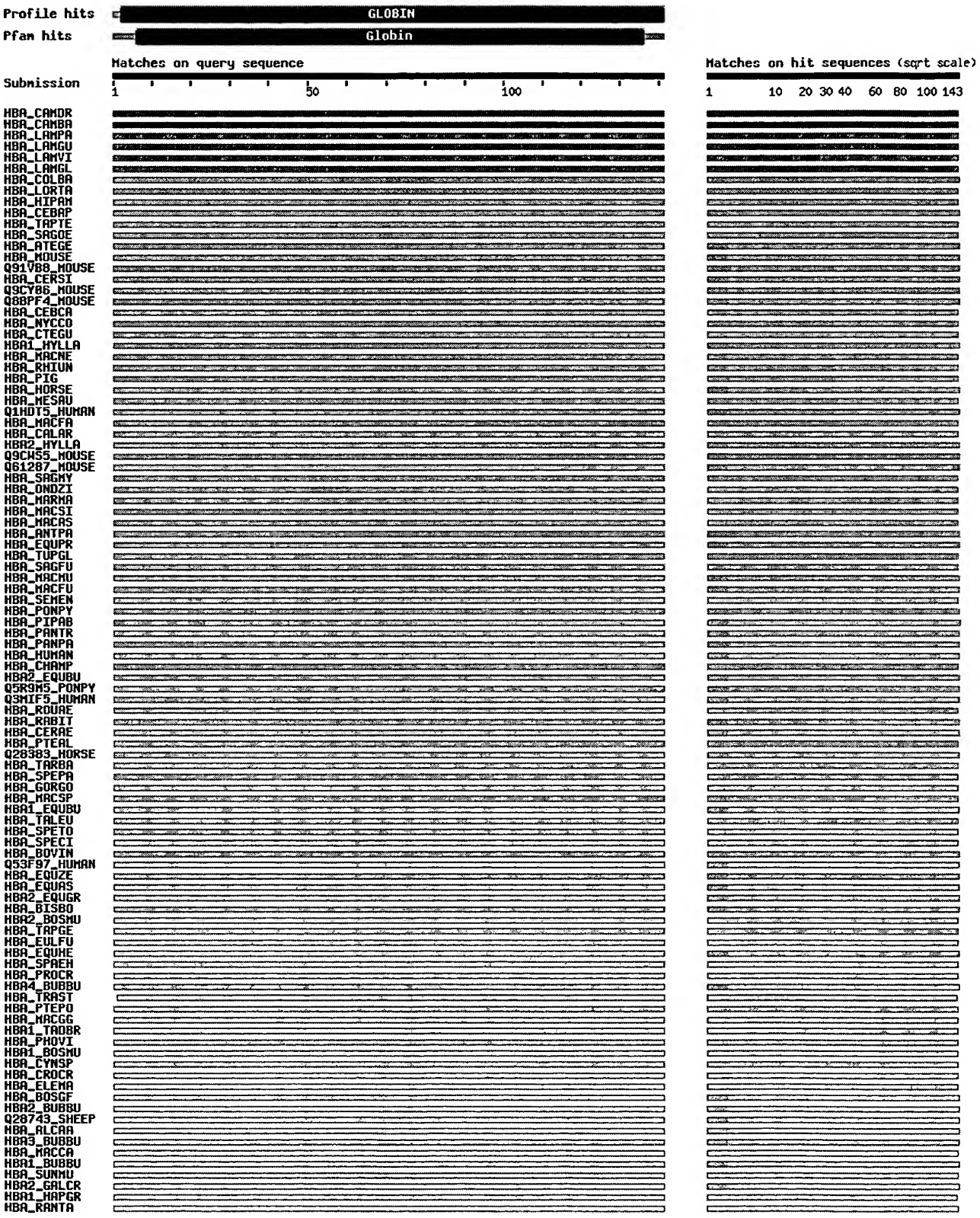
	Db	AC	Description	Score	E-value
☐	sp	P63106	HBA_CAMDR Hemoglobin subunit alpha (Hemoglobin alpha c...	286	2e-77
☐	sp	P63105	HBA_CAMBA Hemoglobin subunit alpha (Hemoglobin alpha c...	286	2e-77
☐	sp	P67816	HBA_LAMPA Hemoglobin subunit alpha (Hemoglobin alpha c...	281	5e-76
☐	sp	P67815	HBA_LAMGU Hemoglobin subunit alpha (Hemoglobin alpha c...	281	5e-76
☐	sp	P07425	HBA_LAMVI Hemoglobin subunit alpha (Hemoglobin alpha c...	280	1e-75
☐	sp	P01973	HBA_LAMGL Hemoglobin subunit alpha (Hemoglobin alpha c...	278	5e-75
☐	sp	P01930	HBA_COLBA Hemoglobin subunit alpha (Hemoglobin alpha c...	254	6e-68
☐	sp	P01938	HBA_LORTA Hemoglobin subunit alpha (Hemoglobin alpha c...	254	8e-68
☐	sp	P19015	HBA_HIPAM Hemoglobin subunit alpha (Hemoglobin alpha c...	253	2e-67
☐	sp	P01928	HBA_CEBAP Hemoglobin subunit alpha (Hemoglobin alpha c...	253	2e-67
☐	sp	P01962	HBA_TAPTE Hemoglobin subunit alpha-1/2 (Hemoglobin alp...	251	4e-67
☐	sp	P67818	HBA_SAGOE Hemoglobin subunit alpha (Hemoglobin alpha c...	251	7e-67
☐	sp	P67817	HBA_ATEGE Hemoglobin subunit alpha (Hemoglobin alpha c...	251	7e-67
☐	sp	P01942	HBA_MOUSE Hemoglobin subunit alpha (Hemoglobin alpha c...	250	9e-67
☐	tr	Q91VB8	_MOUSE 13 days embryo liver cDNA, RIKEN full-length enr...	250	9e-67
☐	sp	P01963	HBA_CERSI Hemoglobin subunit alpha (Hemoglobin alpha c...	249	2e-66
☐	tr	Q9CY06	_MOUSE 13 days embryo liver cDNA, RIKEN full-length enr...	249	2e-66
☐	tr	Q8BPF4	_MOUSE 11 days embryo whole body cDNA, RIKEN full-lengt...	249	2e-66
☐	sp	P07421	HBA_CEBCA Hemoglobin subunit alpha (Hemoglobin alpha c...	249	2e-66
☐	sp	P01937	HBA_NYCCO Hemoglobin subunit alpha (Hemoglobin alpha c...	249	3e-66
☐	sp	P20854	HBA_CTEGU Hemoglobin subunit alpha (Hemoglobin alpha c...	248	3e-66
☐	sp	Q9TS35	HBA1_HYLLA Hemoglobin subunit alpha-1 (Hemoglobin alph...	248	3e-66
☐	sp	P19002	HBA_MACNE Hemoglobin subunit alpha-1/2/3 (Hemoglobin a...	248	4e-66
☐	sp	P09906	HBA_RHIUN Hemoglobin subunit alpha (Hemoglobin alpha c...	248	6e-66
☐	sp	P01965	HBA_PIG Hemoglobin subunit alpha (Hemoglobin alpha cha...	248	6e-66
☐	sp	P01958	HBA_HORSE Hemoglobin subunit alpha (Hemoglobin alpha c...	248	6e-66
☐	sp	P01945	HBA_MESAU Hemoglobin subunit alpha (Hemoglobin alpha c...	247	8e-66
☐	tr	Q1HDT5	_HUMAN Hemoglobin alpha 1-2 hybrid [HBA1] [Homo sapiens...	247	8e-66
☐	sp	P21767	HBA_MACFA Hemoglobin subunit alpha-A/Q/R/T (Hemoglobin...	247	1e-65
☐	sp	P18972	HBA_CALAR Hemoglobin subunit alpha (Hemoglobin alpha c...	247	1e-65
☐	sp	Q9TS34	HBA2_HYLLA Hemoglobin subunit alpha-2 (Hemoglobin alph...	247	1e-65

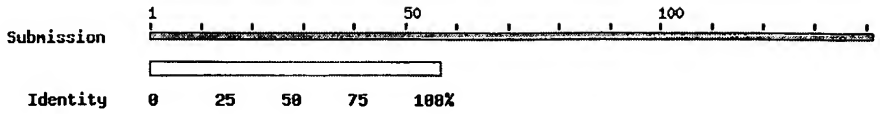
☐	tr Q9CWS5 _MOUSE ES cells cDNA, RIKEN full-length enriched librar...	247	1e-65
☐	tr Q61287 _MOUSE Alpha-globin [Hba-a1] [Mus musculus (Mouse)]	247	1e-65
☐	sp Q7M3B6 HBA_SAGMY Hemoglobin subunit alpha (Hemoglobin alpha c...	246	1e-65
☐	sp P01944 HBA_ONDZI Hemoglobin subunit alpha (Hemoglobin alpha c...	246	1e-65
☐	sp P08852 HBA_MARMA Hemoglobin subunit alpha (Hemoglobin alpha c...	246	1e-65
☐	sp P21768 HBA_MACSI Hemoglobin subunit alpha-1/2 (Hemoglobin alp...	246	1e-65
☐	sp P21766 HBA_MACAS Hemoglobin subunit alpha-1/2/3 (Hemoglobin a...	246	1e-65
☐	sp P14387 HBA_ANTPA Hemoglobin subunit alpha (Hemoglobin alpha c...	246	1e-65
☐	sp Q9XSE9 HBA_EQUPR Hemoglobin subunit alpha (Hemoglobin alpha c...	246	2e-65
☐	sp P01941 HBA_TUPGL Hemoglobin subunit alpha (Hemoglobin alpha c...	246	2e-65
☐	sp P01929 HBA_SAGFU Hemoglobin subunit alpha (Hemoglobin alpha c...	246	2e-65
☐	sp P63108 HBA_MACMU Hemoglobin subunit alpha (Hemoglobin alpha c...	246	2e-65
☐	sp P63107 HBA_MACFU Hemoglobin subunit alpha (Hemoglobin alpha c...	246	2e-65
☐	sp P01924 HBA_SEMEN Hemoglobin subunit alpha (Hemoglobin alpha c...	245	3e-65
☐	sp P06635 HBA_PONPY Hemoglobin subunit alpha (Hemoglobin alpha c...	245	3e-65
☐	sp Q862A7 HBA_PIPAB Hemoglobin subunit alpha (Hemoglobin alpha c...	245	3e-65
☐	sp P69907 HBA_PANTR Hemoglobin subunit alpha (Hemoglobin alpha c...	245	3e-65
☐	sp P69906 HBA_PANPA Hemoglobin subunit alpha (Hemoglobin alpha c...	245	3e-65
☐	sp P69905 HBA_HUMAN Hemoglobin subunit alpha (Hemoglobin alpha c...	245	3e-65
☐	sp Q7M2Y4 HBA_CHAMP Hemoglobin subunit alpha (Hemoglobin alpha c...	245	3e-65
☐	sp Q9TVA3 HBA2_EQUBU Hemoglobin subunit alpha-2 (Hemoglobin alph...	245	3e-65
☐	tr Q5R9M5 _PONPY Hypothetical protein DKFZp468J1717 [DKFZp468J171...	245	3e-65
☐	tr Q3MIF5 _HUMAN Hemoglobin, alpha 1 (HCG1745306, isoform CRA_b) ...	245	3e-65
☐	sp P01956 HBA_ROUAE Hemoglobin subunit alpha (Hemoglobin alpha c...	245	4e-65
☐	sp P01948 HBA_RABIT Hemoglobin subunit alpha-1/2 (Hemoglobin alp...	245	4e-65
☐	sp P01926 HBA_CERAE Hemoglobin subunit alpha (Hemoglobin alpha c...	245	4e-65
☐	sp P14389 HBA_PTEAL Hemoglobin subunit alpha (Hemoglobin alpha c...	244	5e-65
☐	tr Q28383 _HORSE Horse BII alpha-2 globin [Equus caballus (Horse)]	244	5e-65
☐	sp P01940 HBA_TARBA Hemoglobin subunit alpha (Hemoglobin alpha c...	244	6e-65
☐	sp P11750 HBA_SPEPA Hemoglobin subunit alpha (Hemoglobin alpha c...	244	6e-65
☐	sp P01923 HBA_GORGO Hemoglobin subunit alpha (Hemoglobin alpha c...	244	6e-65
☐	sp P07402 HBA_MACSP Hemoglobin subunit alpha-1/2 (Hemoglobin alp...	244	8e-65
☐	sp Q9XSN3 HBA1_EQUBU Hemoglobin subunit alpha-1 (Hemoglobin alph...	244	8e-65
☐	sp P01951 HBA_TALEU Hemoglobin subunit alpha (Hemoglobin alpha c...	243	1e-64
☐	sp P07403 HBA_SPETO Hemoglobin subunit alpha (Hemoglobin alpha c...	243	1e-64
☐	sp P09420 HBA_SPECI Hemoglobin subunit alpha (Hemoglobin alpha c...	243	1e-64
☐	sp P01966 HBA_BOVIN Hemoglobin subunit alpha (Hemoglobin alpha c...	243	1e-64
☐	tr Q53F97 _HUMAN Alpha 2 globin variant (Fragment) [HBA1] [Homo s...	243	1e-64
☐	sp P01960 HBA_EQUZE Hemoglobin subunit alpha (Hemoglobin alpha c...	243	1e-64
☐	sp P01959 HBA_EQUAS Hemoglobin subunit alpha (Hemoglobin alpha c...	243	1e-64
☐	sp Q7JFN6 HBA2_EQUGR Hemoglobin subunit alpha-2 (Hemoglobin alph...	243	1e-64
☐	sp P09423 HBA_BISBO Hemoglobin subunit alpha-I/II (Hemoglobin al...	242	2e-64
☐	sp P01968 HBA2_BOSMU Hemoglobin subunit alpha-2 (Hemoglobin alph...	242	2e-64
☐	sp P28780 HBA_TAPGE Hemoglobin subunit alpha (Hemoglobin alpha c...	242	3e-64
☐	sp P01936 HBA_EULFU Hemoglobin subunit alpha (Hemoglobin alpha c...	242	3e-64
☐	sp P01961 HBA_EQUHE Hemoglobin subunit alpha-1/2 (Hemoglobin alp...	242	3e-64
☐	sp P01943 HBA_SPAEH Hemoglobin subunit alpha (Hemoglobin alpha c...	241	4e-64
☐	sp P23019 HBA_PROCR Hemoglobin subunit alpha (Hemoglobin alpha c...	241	4e-64
☐	sp Q9XSK1 HBA4_BUBBU Hemoglobin subunit alpha-4 (Hemoglobin alph...	241	4e-64
☐	sp P04237 HBA_TRAST Hemoglobin subunit alpha (Hemoglobin alpha c...	241	5e-64
☐	sp P14390 HBA_PTEPO Hemoglobin subunit alpha (Hemoglobin alpha c...	241	7e-64
☐	sp P24659 HBA_MACGG Hemoglobin subunit alpha-1/2 (Hemoglobin alp...	241	7e-64
☐	sp P11755 HBA1_TADBR Hemoglobin subunit alpha-1 (Hemoglobin alph...	241	7e-64
☐	sp P09908 HBA_PHOVI Hemoglobin subunit alpha (Hemoglobin alpha c...	240	9e-64
☐	sp P01967 HBA1_BOSMU Hemoglobin subunit alpha-1 (Hemoglobin alph...	240	9e-64
☐	sp P11753 HBA_CYNSP Hemoglobin subunit alpha (Hemoglobin alpha c...	240	1e-63
☐	sp P18973 HBA_CROCR Hemoglobin subunit alpha (Hemoglobin alpha c...	240	1e-63
☐	sp P01954 HBA_ELEMA Hemoglobin subunit alpha (Hemoglobin alpha c...	239	2e-63
☐	sp P01969 HBA_BOSGF Hemoglobin subunit alpha (Hemoglobin alpha c...	239	2e-63
☐	sp Q9TSN8 HBA2_BUBBU Hemoglobin subunit alpha-2 (Hemoglobin alph...	239	2e-63
☐	tr Q28743 _SHEEP Alpha globin chain [Ovis aries (Sheep)]	239	2e-63
☐	sp P01971 HBA_ALCAA Hemoglobin subunit alpha (Hemoglobin alpha c...	239	2e-63
☐	sp Q9TSN9 HBA3_BUBBU Hemoglobin subunit alpha-3 (Hemoglobin alph...	239	2e-63
☐	sp P09839 HBA_MACCA Hemoglobin subunit alpha (Hemoglobin alpha c...	239	3e-63
☐	sp Q9TSN7 HBA1_BUBBU Hemoglobin subunit alpha-1 (Hemoglobin alph...	239	3e-63
☐	sp P01950 HBA_SUNMU Hemoglobin subunit alpha (Hemoglobin alpha c...	238	3e-63

- sp P01939 HBA2_GALCR Hemoglobin subunit alpha-B (Hemoglobin alph... 238 3e-63
- sp Q7M3B8 HBA1_HAPGR Hemoglobin subunit alpha-1 (Hemoglobin alph... 238 3e-63
- sp P21379 HBA_RANTA Hemoglobin subunit alpha (Hemoglobin alpha c... 238 5e-63

Graphical overview of the alignments

Click here to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs
(Help) (use ScanProsite for more details about PROSITE matches)





Alignments

sp P63106 Hemoglobin subunit alpha (Hemoglobin alpha chain) (Alpha-globin) 141 AA
HBA_CAMDR [HBA] [Camelus dromedarius (Dromedary) (Arabian camel)] align

Score = 286 bits (731), Expect = 2e-77
Identities = 141/141 (100%), Positives = 141/141 (100%)

```
Query: 1   VLSSKDKTNVKTAFGKIGGHAAEYGAEALERMFLGFPTTKTYFPHFDLSHGSAQVKAHGK 60
           VLSSKDKTNVKTAFGKIGGHAAEYGAEALERMFLGFPTTKTYFPHFDLSHGSAQVKAHGK
Sbjct: 1   VLSSKDKTNVKTAFGKIGGHAAEYGAEALERMFLGFPTTKTYFPHFDLSHGSAQVKAHGK 60

Query: 61  KVGDALTKAADHLDDLPSALSALSDLHAHKLRVDPVNFKLLSHCLLVTVAAHHPGDFTPS 120
           KVGDALTKAADHLDDLPSALSALSDLHAHKLRVDPVNFKLLSHCLLVTVAAHHPGDFTPS
Sbjct: 61  KVGDALTKAADHLDDLPSALSALSDLHAHKLRVDPVNFKLLSHCLLVTVAAHHPGDFTPS 120

Query: 121 VHASLDKFLANVSTVLTSKYR 141
           VHASLDKFLANVSTVLTSKYR
Sbjct: 121 VHASLDKFLANVSTVLTSKYR 141
```

sp P63105 Hemoglobin subunit alpha (Hemoglobin alpha chain) (Alpha-globin) 141 AA
HBA_CAMBA [HBA] [Camelus bactrianus (Bactrian camel)] align

Score = 286 bits (731), Expect = 2e-77
Identities = 141/141 (100%), Positives = 141/141 (100%)

```
Query: 1   VLSSKDKTNVKTAFGKIGGHAAEYGAEALERMFLGFPTTKTYFPHFDLSHGSAQVKAHGK 60
           VLSSKDKTNVKTAFGKIGGHAAEYGAEALERMFLGFPTTKTYFPHFDLSHGSAQVKAHGK
Sbjct: 1   VLSSKDKTNVKTAFGKIGGHAAEYGAEALERMFLGFPTTKTYFPHFDLSHGSAQVKAHGK 60

Query: 61  KVGDALTKAADHLDDLPSALSALSDLHAHKLRVDPVNFKLLSHCLLVTVAAHHPGDFTPS 120
           KVGDALTKAADHLDDLPSALSALSDLHAHKLRVDPVNFKLLSHCLLVTVAAHHPGDFTPS
Sbjct: 61  KVGDALTKAADHLDDLPSALSALSDLHAHKLRVDPVNFKLLSHCLLVTVAAHHPGDFTPS 120

Query: 121 VHASLDKFLANVSTVLTSKYR 141
           VHASLDKFLANVSTVLTSKYR
Sbjct: 121 VHASLDKFLANVSTVLTSKYR 141
```

sp P67816 Hemoglobin subunit alpha (Hemoglobin alpha chain) (Alpha-globin) 141 AA
HBA_LAMPA [HBA] [Lama guanicoe pacos (Alpaca) (Lama pacos)] align

Score = 281 bits (719), Expect = 5e-76
Identities = 137/141 (97%), Positives = 140/141 (99%)

```
Query: 1   VLSSKDKTNVKTAFGKIGGHAAEYGAEALERMFLGFPTTKTYFPHFDLSHGSAQVKAHGK 60
           VLSSKDK N+KTAFGKIGGHAA+YGAEALERMFLGFPTTKTYFPHFDLSHGSAQVKAHGK
Sbjct: 1   VLSSKDKANIKTAFGKIGGHAADYGAEALERMFLGFPTTKTYFPHFDLSHGSAQVKAHGK 60

Query: 61  KVGDALTKAADHLDDLPSALSALSDLHAHKLRVDPVNFKLLSHCLLVTVAAHHPGDFTPS 120
           KVGDALTKAADHLDDLPSALSALSDLHAHKLRVDPVNFKLLSHCLLVTVAAHHPGDFTP+
Sbjct: 61  KVGDALTKAADHLDDLPSALSALSDLHAHKLRVDPVNFKLLSHCLLVTVAAHHPGDFTPA 120

Query: 121 VHASLDKFLANVSTVLTSKYR 141
           VHASLDKFLANVSTVLTSKYR
Sbjct: 121 VHASLDKFLANVSTVLTSKYR 141
```

sp P67815 Hemoglobin subunit alpha (Hemoglobin alpha chain) (Alpha-globin) 141 AA
HBA_LAMGU [HBA] [Lama guanicoe (Guanaco)] align

```
 Score =  281 bits (719), Expect = 5e-76
 Identities = 137/141 (97%), Positives = 140/141 (99%)

Query: 1   VLSSKDKTNVKTAFGKIGGHAAEYGAEALERMFLGFPTTKTYFPHFDLSHGSAQVKAHGK 60
           VLSSKDK N+KTAFGKIGGHAA+YGAEALERMFLGFPTTKTYFPHFDLSHGSAQVKAHGK
Sbjct: 1   VLSSKDKANIKTAFGKIGGHAADYGAEALERMFLGFPTTKTYFPHFDLSHGSAQVKAHGK 60

Query: 61  KVGDALTKAADHLDDLPSALSALSDLHAHKLRVDPVNFKLLSHCLLVTVAAHHPGDFTPS 120
           KVGDALTKAADHLDDLPSALSALSDLHAHKLRVDPVNFKLLSHCLLVTVAAHHPGDFTP+
Sbjct: 61  KVGDALTKAADHLDDLPSALSALSDLHAHKLRVDPVNFKLLSHCLLVTVAAHHPGDFTPA 120

Query: 121 VHASLDKFLANVSTVLTSKYR 141
           VHASLDKFLANVSTVLTSKYR
Sbjct: 121 VHASLDKFLANVSTVLTSKYR 141
```

sp P07425 HBA_LAMVI **Hemoglobin subunit alpha (Hemoglobin alpha chain) (Alpha-globin) [HBA] [Lama vicugna (Vicugna) (Vicugna vicugna)]** 141 AA align

```
 Score =  280 bits (716), Expect = 1e-75
 Identities = 137/141 (97%), Positives = 139/141 (98%)

Query: 1   VLSSKDKTNVKTAFGKIGGHAAEYGAEALERMFLGFPTTKTYFPHFDLSHGSAQVKAHGK 60
           VLSSKDK NVKTAFGKIGGHAA+YGAEALERMFLGFPTTKTYFPHFDLSHGSAQVKAHGK
Sbjct: 1   VLSSKDKANVKTAFGKIGGHAADYGAEALERMFLGFPTTKTYFPHFDLSHGSAQVKAHGK 60

Query: 61  KVGDALTKAADHLDDLPSALSALSDLHAHKLRVDPVNFKLLSHCLLVTVAAHHPGDFTPS 120
           KVGDALTKAADHLDDLPSALSALSDLHAHKLRVDPVNFKLLSHCLLVTVAAHHPGDFTP+
Sbjct: 61  KVGDALTKAADHLDDLPSALSALSDLHAHKLRVDPVNFKLLSHCLLVTVAAHHPGDFTPA 120

Query: 121 VHASLDKFLANVSTVLTSKYR 141
           VHASLDKFL NVSTVLTSKYR
Sbjct: 121 VHASLDKFLTNVSTVLTSKYR 141
```

sp P01973 HBA_LAMGL **Hemoglobin subunit alpha (Hemoglobin alpha chain) (Alpha-globin) [HBA] [Lama glama (Llama)]** 141 AA align

```
 Score =  278 bits (710), Expect = 5e-75
 Identities = 136/141 (96%), Positives = 139/141 (98%)

Query: 1   VLSSKDKTNVKTAFGKIGGHAAEYGAEALERMFLGFPTTKTYFPHFDLSHGSAQVKAHGK 60
           VLSSKDK N+KTAFGKIGGHAA+YGAEALERMFLGFPTTKTYFPHFDLSHGSAQVKAHGK
Sbjct: 1   VLSSKDKANIKTAFGKIGGHAADYGAEALERMFLGFPTTKTYFPHFDLSHGSAQVKAHGK 60

Query: 61  KVGDALTKAADHLDDLPSALSALSDLHAHKLRVDPVNFKLLSHCLLVTVAAHHPGDFTPS 120
           KVGDALTKAADHLDDLPSALSALSDLHAHKLRVDPVNFKLLSHCLLVTVAAHHPGDFTP+
Sbjct: 61  KVGDALTKAADHLDDLPSALSALSDLHAHKLRVDPVNFKLLSHCLLVTVAAHHPGDFTPA 120

Query: 121 VHASLDKFLANVSTVLTSKYR 141
           V ASLDKFLANVSTVLTSKYR
Sbjct: 121 VDASLDKFLANVSTVLTSKYR 141
```

sp P01930 HBA_COLBA **Hemoglobin subunit alpha (Hemoglobin alpha chain) (Alpha-globin) [HBA] [Colobus badius (Red colobus) (Procolobus badius)]** 142 AA align

```
 Score =  254 bits (649), Expect = 6e-68
 Identities = 123/141 (87%), Positives = 131/141 (92%)

Query: 1   VLSSKDKTNVKTAFGKIGGHAAEYGAEALERMFLGFPTTKTYFPHFDLSHGSAQVKAHGK 60
           VLS  DKTNVKTA+GK+GGH  EYGAEALERMFL FPTTKTYFPHFDLSHGSAQVK HGK
Sbjct: 2   VLSPADKTNVKTAWGKVGGHGGEYGAEALERMFLSFPTTKTYFPHFDLSHGSAQVKGHGK 61

Query: 61  KVGDALTKAADHLDDLPSALSALSDLHAHKLRVDPVNFKLLSHCLLVTVAAHHPGDFTPS 120
           KV DALT AA H+DD+PSALSALSDLHAHKLRVDPVNFKLLSHCLLVT+AAHHP +FTP+
Sbjct: 62  KVADALTLAAAHVDDMPSALSALSDLHAHKLRVDPVNFKLLSHCLLVTLAAHHPAEFTPA 121

Query: 121 VHASLDKFLANVSTVLTSKYR 141
           VHASLDKFLA+VSTVLTSKYR
Sbjct: 122 VHASLDKFLASVSTVLTSKYR 142
```

Ex. I

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Welcome to the SIB BLAST Network Service

If results of this search are reported or published, please mention that
the computation was performed at the SIB using the BLAST network service.
The SIB BLAST network service uses a server developed at SIB and the NCBI
BLAST 2 software.

In case of problems, please read the online BLAST help.
If your question is not covered, please contact <helpdesk@expasy.org>.

NCBI BLAST program reference [PMID:9254694]:
Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W.,
Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein
database search programs. Nucleic Acids Res. 25:3389-3402(1997).

==========

Query: 147 AA
Date run: 2007-02-09 18:42:06 UTC+0100 on blast01.vital-it.ch
Program: NCBI BLASTP 2.2.15 [Oct-15-2006]
Database: UniProtKB Mammalia
240,475 sequences; 91,865,493 total letters
UniProt Knowledgebase Release 9.6 consists of:
UniProtKB/Swiss-Prot Release 51.6 of 06-Feb-2007: 257964 entries
UniProtKB/TrEMBL Release 34.6 of 06-Feb-2007: 3745801 entries

Taxonomic view | NiceBlast view | Printable view

List of potentially matching sequences

Send selected sequences to Clustal W (multiple alignment) Submit Query Select up to...

☐ Include query sequence

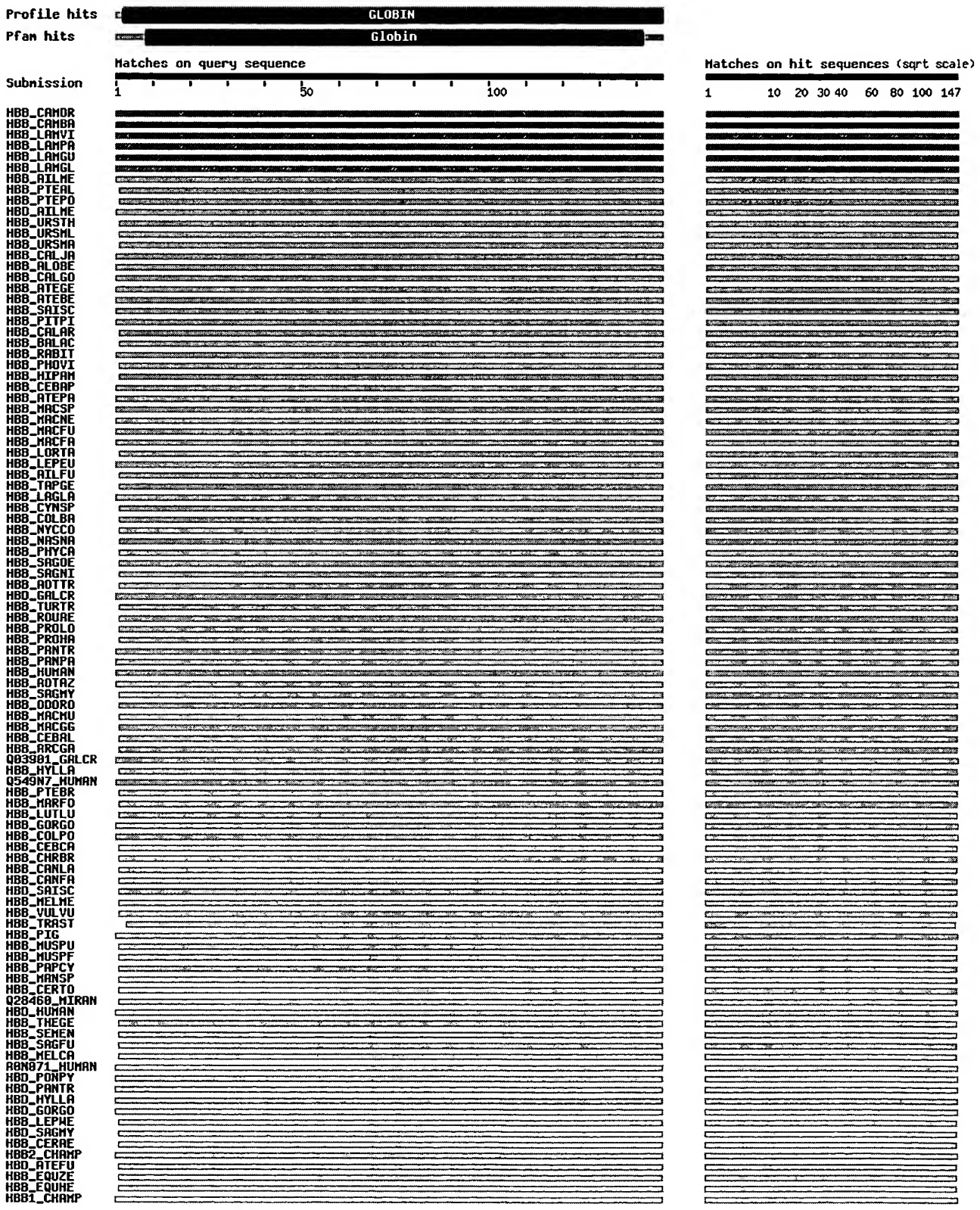
	Db AC	Description	Score	E-value
☐	sp P68231	HBB_CAMDR Hemoglobin subunit beta (Hemoglobin beta cha...	303	2e-82
☐	sp P68230	HBB_CAMBA Hemoglobin subunit beta (Hemoglobin beta cha...	303	2e-82
☐	sp P68227	HBB_LAMVI Hemoglobin subunit beta (Hemoglobin beta cha...	298	4e-81
☐	sp P68228	HBB_LAMPA Hemoglobin subunit beta (Hemoglobin beta cha...	298	4e-81
☐	sp P68229	HBB_LAMGU Hemoglobin subunit beta (Hemoglobin beta cha...	298	4e-81
☐	sp P68226	HBB_LAMGL Hemoglobin subunit beta (Hemoglobin beta cha...	298	4e-81
☐	sp P18983	HBB_AILME Hemoglobin subunit beta (Hemoglobin beta cha...	265	4e-71
☐	sp P14391	HBB_PTEAL Hemoglobin subunit beta (Hemoglobin beta cha...	264	7e-71
☐	sp P14392	HBB_PTEPO Hemoglobin subunit beta (Hemoglobin beta cha...	264	9e-71
☐	sp Q5XLE5	HBD_AILME Hemoglobin subunit delta (Hemoglobin delta c...	263	1e-70
☐	sp P68012	HBB_URSTH Hemoglobin subunit beta (Hemoglobin beta cha...	262	3e-70
☐	sp P68013	HBB_URSML Hemoglobin subunit beta (Hemoglobin beta cha...	262	3e-70
☐	sp P68011	HBB_URSMA Hemoglobin subunit beta (Hemoglobin beta cha...	262	3e-70
☐	sp Q6WN28	HBB_CALJA Hemoglobin subunit beta (Hemoglobin beta cha...	262	3e-70
☐	sp Q6WN29	HBB_ALOBE Hemoglobin subunit beta (Hemoglobin beta cha...	262	3e-70
☐	sp Q6WN21	HBB_CALGO Hemoglobin subunit beta (Hemoglobin beta cha...	261	6e-70
☐	sp P68232	HBB_ATEGE Hemoglobin subunit beta (Hemoglobin beta cha...	261	6e-70
☐	sp P68234	HBB_ATEBE Hemoglobin subunit beta (Hemoglobin beta cha...	261	6e-70
☐	sp P02036	HBB_SAISC Hemoglobin subunit beta (Hemoglobin beta cha...	261	7e-70
☐	sp Q6WN27	HBB_PITPI Hemoglobin subunit beta (Hemoglobin beta cha...	260	1e-69
☐	sp P18985	HBB_CALAR Hemoglobin subunit beta (Hemoglobin beta cha...	260	1e-69
☐	sp P18984	HBB_BALAC Hemoglobin subunit beta (Hemoglobin beta cha...	260	1e-69
☐	sp P02057	HBB_RABIT Hemoglobin subunit beta-1/2 (Hemoglobin beta...	259	2e-69
☐	sp P09909	HBB_PHOVI Hemoglobin subunit beta (Hemoglobin beta cha...	259	2e-69
☐	sp P19016	HBB_HIPAM Hemoglobin subunit beta (Hemoglobin beta cha...	259	2e-69
☐	sp P67821	HBB_CEBAP Hemoglobin subunit beta (Hemoglobin beta cha...	259	2e-69
☐	sp Q6WN22	HBB_ATEPA Hemoglobin subunit beta (Hemoglobin beta cha...	259	2e-69
☐	sp P68224	HBB_MACSP Hemoglobin subunit beta (Hemoglobin beta cha...	259	2e-69
☐	sp P68225	HBB_MACNE Hemoglobin subunit beta (Hemoglobin beta cha...	259	2e-69
☐	sp P68222	HBB_MACFU Hemoglobin subunit beta (Hemoglobin beta cha...	259	2e-69
☐	sp P68223	HBB_MACFA Hemoglobin subunit beta (Hemoglobin beta cha...	259	2e-69

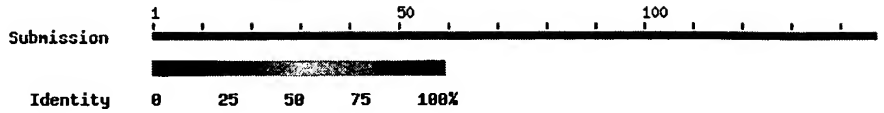
sp P02048 HBB_LORTA Hemoglobin subunit beta (Hemoglobin beta cha...	259	2e-69
sp P08535 HBB_LEPEU Hemoglobin subunit beta (Hemoglobin beta cha...	259	2e-69
sp P18982 HBB_AILFU Hemoglobin subunit beta (Hemoglobin beta cha...	259	2e-69
sp P28781 HBB_TAPGE Hemoglobin subunit beta (Hemoglobin beta cha...	259	3e-69
sp Q6WN25 HBB_LAGLA Hemoglobin subunit beta (Hemoglobin beta cha...	259	3e-69
sp P11754 HBB_CYNSP Hemoglobin subunit beta (Hemoglobin beta cha...	259	3e-69
sp P02033 HBB_COLBA Hemoglobin subunit beta (Hemoglobin beta cha...	259	3e-69
sp P02049 HBB_NYCCO Hemoglobin subunit beta (Hemoglobin beta cha...	258	4e-69
sp P26916 HBB_NASNA Hemoglobin subunit beta (Hemoglobin beta cha...	258	4e-69
sp P09905 HBB_PHYCA Hemoglobin subunit beta-1/2 (Hemoglobin beta...	258	5e-69
sp P68055 HBB_SAGOE Hemoglobin subunit beta (Hemoglobin beta cha...	257	8e-69
sp P68054 HBB_SAGNI Hemoglobin subunit beta (Hemoglobin beta cha...	257	8e-69
sp P02035 HBB_AOTTR Hemoglobin subunit beta (Hemoglobin beta cha...	257	8e-69
sp Q03902 HBD_GALCR Hemoglobin subunit delta (Hemoglobin delta c...	257	1e-68
sp P18990 HBB_TURTR Hemoglobin subunit beta (Hemoglobin beta cha...	257	1e-68
sp P02058 HBB_ROUAE Hemoglobin subunit beta (Hemoglobin beta cha...	256	1e-68
sp P18989 HBB_PROLO Hemoglobin subunit beta (Hemoglobin beta cha...	256	1e-68
sp P02086 HBB_PROHA Hemoglobin subunit beta (Hemoglobin beta cha...	256	1e-68
sp P68873 HBB_PANTR Hemoglobin subunit beta (Hemoglobin beta cha...	256	1e-68
sp P68872 HBB_PANPA Hemoglobin subunit beta (Hemoglobin beta cha...	256	1e-68
sp P68871 HBB_HUMAN Hemoglobin subunit beta (Hemoglobin beta cha...	256	1e-68
sp Q6WN26 HBB_AOTAZ Hemoglobin subunit beta (Hemoglobin beta cha...	256	1e-68
sp P02038 HBB_SAGMY Hemoglobin subunit beta (Hemoglobin beta cha...	256	2e-68
sp P68046 HBB_ODORO Hemoglobin subunit beta (Hemoglobin beta cha...	256	2e-68
sp P02026 HBB_MACMU Hemoglobin subunit beta (Hemoglobin beta cha...	256	2e-68
sp P24660 HBB_MACGG Hemoglobin subunit beta (Hemoglobin beta cha...	256	2e-68
sp P02040 HBB_CEBAL Hemoglobin subunit beta (Hemoglobin beta cha...	256	2e-68
sp P68047 HBB_ARCGA Hemoglobin subunit beta (Hemoglobin beta cha...	256	2e-68
tr Q03901 _GALCR Beta-globin protein [beta-globin] [Galago crassi...	256	2e-68
sp P02025 HBB_HYLLA Hemoglobin subunit beta (Hemoglobin beta cha...	256	2e-68
tr Q549N7 _HUMAN Mutant beta-globin [HBB] [Homo sapiens (Human)]	256	2e-68
sp P68052 HBB_PTEBR Hemoglobin subunit beta (Hemoglobin beta cha...	255	3e-68
sp P68053 HBB_MARFO Hemoglobin subunit beta (Hemoglobin beta cha...	255	3e-68
sp P10893 HBB_LUTLU Hemoglobin subunit beta (Hemoglobin beta cha...	255	3e-68
sp P02024 HBB_GORGO Hemoglobin subunit beta (Hemoglobin beta cha...	255	3e-68
sp P19885 HBB_COLPO Hemoglobin subunit beta (Hemoglobin beta cha...	255	3e-68
sp P67822 HBB_CEBCA Hemoglobin subunit beta (Hemoglobin beta cha...	255	3e-68
sp P60526 HBB_CHRBR Hemoglobin subunit beta (Hemoglobin beta cha...	255	4e-68
sp P60525 HBB_CANLA Hemoglobin subunit beta (Hemoglobin beta cha...	255	4e-68
sp P60524 HBB_CANFA Hemoglobin subunit beta (Hemoglobin beta cha...	255	4e-68
sp P02047 HBD_SAISC Hemoglobin subunit delta (Hemoglobin delta c...	254	5e-68
sp P02055 HBB_MELME Hemoglobin subunit beta (Hemoglobin beta cha...	254	5e-68
sp P21201 HBB_VULVU Hemoglobin subunit beta (Hemoglobin beta cha...	254	7e-68
sp P04245 HBB_TRAST Hemoglobin subunit beta (Hemoglobin beta cha...	254	7e-68
sp P02067 HBB_PIG Hemoglobin subunit beta (Hemoglobin beta chain...	254	7e-68
sp P68045 HBB_MUSPU Hemoglobin subunit beta (Hemoglobin beta cha...	254	7e-68
sp P68044 HBB_MUSPF Hemoglobin subunit beta (Hemoglobin beta cha...	254	7e-68
sp P02030 HBB_PAPCY Hemoglobin subunit beta (Hemoglobin beta cha...	254	9e-68
sp P08259 HBB_MANSP Hemoglobin subunit beta (Hemoglobin beta cha...	254	9e-68
sp P02031 HBB_CERTO Hemoglobin subunit beta (Hemoglobin beta cha...	253	1e-67
tr Q28460 _MIRAN MRNA, . (Fragment) [Mirounga angustirostris (Nor...	253	1e-67
sp P02042 HBD_HUMAN Hemoglobin subunit delta (Hemoglobin delta c...	253	2e-67
sp P02029 HBB_THEGE Hemoglobin subunit beta (Hemoglobin beta cha...	253	2e-67
sp P02032 HBB_SEMEN Hemoglobin subunit beta (Hemoglobin beta cha...	253	2e-67
sp P02039 HBB_SAGFU Hemoglobin subunit beta (Hemoglobin beta cha...	253	2e-67
sp P15449 HBB_MELCA Hemoglobin subunit beta (Hemoglobin beta cha...	253	2e-67
tr A0N071 _HUMAN Delta-globin chain (Hemoglobin delta) [HBD] [Hom...	253	2e-67
sp P61775 HBD_PONPY Hemoglobin subunit delta (Hemoglobin delta c...	253	2e-67
sp P61772 HBD_PANTR Hemoglobin subunit delta (Hemoglobin delta c...	253	2e-67
sp P61774 HBD_HYLLA Hemoglobin subunit delta (Hemoglobin delta c...	253	2e-67
sp P61773 HBD_GORGO Hemoglobin subunit delta (Hemoglobin delta c...	253	2e-67
sp P15166 HBB_LEPWE Hemoglobin subunit beta (Hemoglobin beta cha...	252	3e-67
sp P68014 HBD_SAGMY Hemoglobin subunit delta (Hemoglobin delta c...	252	3e-67
sp P02028 HBB_CERAE Hemoglobin subunit beta (Hemoglobin beta cha...	252	3e-67
sp Q7M2Y5 HBB2_CHAMP Hemoglobin subunit beta-2 (Hemoglobin beta-...	251	4e-67
sp P33499 HBD_ATEFU Hemoglobin subunit delta (Hemoglobin delta c...	251	6e-67

☐ sp P67824 HBB_EQUZE Hemoglobin subunit beta (Hemoglobin beta cha... 251 6e-67
☐ sp P67823 HBB_EQUHE Hemoglobin subunit beta (Hemoglobin beta cha... 251 6e-67
☐ sp P68087 HBB1_CHAMP Hemoglobin subunit beta-1 (Hemoglobin beta-... 251 6e-67

Graphical overview of the alignments

Click here to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs
(Help) (use ScanProsite for more details about PROSITE matches)





Alignments

sp P68231 HBB_CAMDR **Hemoglobin subunit beta (Hemoglobin beta chain) (Beta-globin) [HBB] [Camelus dromedarius (Dromedary) (Arabian camel)]** 147 AA align

Score = 303 bits (775), Expect = 2e-82
Identities = 147/147 (100%), Positives = 147/147 (100%)

```
Query: 1   MVHLSGDEKNAVHGLWSKVKVDEVGGEALGRLLVVYPWTRRFFESFGDLSTADAVMNNPK 60
           MVHLSGDEKNAVHGLWSKVKVDEVGGEALGRLLVVYPWTRRFFESFGDLSTADAVMNNPK
Sbjct: 1   MVHLSGDEKNAVHGLWSKVKVDEVGGEALGRLLVVYPWTRRFFESFGDLSTADAVMNNPK 60

Query: 61  VKAHGSKVLNSFGDGLNHLDNLKGTYAKLSELHCDKLHVDPENFRLLGNVLVVVLARHFG 120
           VKAHGSKVLNSFGDGLNHLDNLKGTYAKLSELHCDKLHVDPENFRLLGNVLVVVLARHFG
Sbjct: 61  VKAHGSKVLNSFGDGLNHLDNLKGTYAKLSELHCDKLHVDPENFRLLGNVLVVVLARHFG 120

Query: 121 KEFTPDLQAAYQKVVAGVANALAHRYH 147
           KEFTPDLQAAYQKVVAGVANALAHRYH
Sbjct: 121 KEFTPDLQAAYQKVVAGVANALAHRYH 147
```

sp P68230 HBB_CAMBA **Hemoglobin subunit beta (Hemoglobin beta chain) (Beta-globin) [HBB] [Camelus bactrianus (Bactrian camel)]** 147 AA align

Score = 303 bits (775), Expect = 2e-82
Identities = 147/147 (100%), Positives = 147/147 (100%)

```
Query: 1   MVHLSGDEKNAVHGLWSKVKVDEVGGEALGRLLVVYPWTRRFFESFGDLSTADAVMNNPK 60
           MVHLSGDEKNAVHGLWSKVKVDEVGGEALGRLLVVYPWTRRFFESFGDLSTADAVMNNPK
Sbjct: 1   MVHLSGDEKNAVHGLWSKVKVDEVGGEALGRLLVVYPWTRRFFESFGDLSTADAVMNNPK 60

Query: 61  VKAHGSKVLNSFGDGLNHLDNLKGTYAKLSELHCDKLHVDPENFRLLGNVLVVVLARHFG 120
           VKAHGSKVLNSFGDGLNHLDNLKGTYAKLSELHCDKLHVDPENFRLLGNVLVVVLARHFG
Sbjct: 61  VKAHGSKVLNSFGDGLNHLDNLKGTYAKLSELHCDKLHVDPENFRLLGNVLVVVLARHFG 120

Query: 121 KEFTPDLQAAYQKVVAGVANALAHRYH 147
           KEFTPDLQAAYQKVVAGVANALAHRYH
Sbjct: 121 KEFTPDLQAAYQKVVAGVANALAHRYH 147
```

sp P68227 HBB_LAMVI **Hemoglobin subunit beta (Hemoglobin beta chain) (Beta-globin) [HBB] [Lama vicugna (Vicugna) (Vicugna vicugna)]** 147 AA align

Score = 298 bits (763), Expect = 4e-81
Identities = 145/147 (98%), Positives = 147/147 (100%)

```
Query: 1   MVHLSGDEKNAVHGLWSKVKVDEVGGEALGRLLVVYPWTRRFFESFGDLSTADAVMNNPK 60
           MV+LSGDEKNAVHGLWSKVKVDEVGGEALGRLLVVYPWTRRFFESFGDLSTADAVMNNPK
Sbjct: 1   MVNLSGDEKNAVHGLWSKVKVDEVGGEALGRLLVVYPWTRRFFESFGDLSTADAVMNNPK 60

Query: 61  VKAHGSKVLNSFGDGLNHLDNLKGTYAKLSELHCDKLHVDPENFRLLGNVLVVVLARHFG 120
           VKAHGSKVLNSFGDGL+HLDNLKGTYAKLSELHCDKLHVDPENFRLLGNVLVVVLARHFG
Sbjct: 61  VKAHGSKVLNSFGDGLSHLDNLKGTYAKLSELHCDKLHVDPENFRLLGNVLVVVLARHFG 120

Query: 121 KEFTPDLQAAYQKVVAGVANALAHRYH 147
           KEFTPDLQAAYQKVVAGVANALAHRYH
Sbjct: 121 KEFTPDLQAAYQKVVAGVANALAHRYH 147
```

sp P68228 HBB_LAMPA **Hemoglobin subunit beta (Hemoglobin beta chain) (Beta-globin) [HBB] [Lama guanicoe pacos (Alpaca) (Lama pacos)]** 147 AA align

```
 Score =  298 bits (763), Expect = 4e-81
 Identities = 145/147 (98%), Positives = 147/147 (100%)

Query: 1   MVHLSGDEKNAVHGLWSKVKVDEVGGEALGRLLVVYPWTRRFFESFGDLSTADAVMNNPK 60
           MV+LSGDEKNAVHGLWSKVKVDEVGGEALGRLLVVYPWTRRFFESFGDLSTADAVMNNPK
Sbjct: 1   MVNLSGDEKNAVHGLWSKVKVDEVGGEALGRLLVVYPWTRRFFESFGDLSTADAVMNNPK 60

Query: 61  VKAHGSKVLNSFGDGLNHLDNLKGTYAKLSELHCDKLHVDPENFRLLGNVLVVVLARHFG 120
           VKAHGSKVLNSFGDGL+HLDNLKGTYAKLSELHCDKLHVDPENFRLLGNVLVVVLARHFG
Sbjct: 61  VKAHGSKVLNSFGDGLSHLDNLKGTYAKLSELHCDKLHVDPENFRLLGNVLVVVLARHFG 120

Query: 121 KEFTPDLQAAYQKVVAGVANALAHRYH 147
           KEFTPDLQAAYQKVVAGVANALAHRYH
Sbjct: 121 KEFTPDLQAAYQKVVAGVANALAHRYH 147
```

sp P68229 **Hemoglobin subunit beta (Hemoglobin beta chain) (Beta-globin) [HBB]** 147 AA
HBB_LAMGU **[Lama guanicoe (Guanaco)]** align

```
 Score =  298 bits (763), Expect = 4e-81
 Identities = 145/147 (98%), Positives = 147/147 (100%)

Query: 1   MVHLSGDEKNAVHGLWSKVKVDEVGGEALGRLLVVYPWTRRFFESFGDLSTADAVMNNPK 60
           MV+LSGDEKNAVHGLWSKVKVDEVGGEALGRLLVVYPWTRRFFESFGDLSTADAVMNNPK
Sbjct: 1   MVNLSGDEKNAVHGLWSKVKVDEVGGEALGRLLVVYPWTRRFFESFGDLSTADAVMNNPK 60

Query: 61  VKAHGSKVLNSFGDGLNHLDNLKGTYAKLSELHCDKLHVDPENFRLLGNVLVVVLARHFG 120
           VKAHGSKVLNSFGDGL+HLDNLKGTYAKLSELHCDKLHVDPENFRLLGNVLVVVLARHFG
Sbjct: 61  VKAHGSKVLNSFGDGLSHLDNLKGTYAKLSELHCDKLHVDPENFRLLGNVLVVVLARHFG 120

Query: 121 KEFTPDLQAAYQKVVAGVANALAHRYH 147
           KEFTPDLQAAYQKVVAGVANALAHRYH
Sbjct: 121 KEFTPDLQAAYQKVVAGVANALAHRYH 147
```

sp P68226 **Hemoglobin subunit beta (Hemoglobin beta chain) (Beta-globin) [HBB]** 147 AA
HBB_LAMGL **[Lama glama (Llama)]** align

```
 Score =  298 bits (763), Expect = 4e-81
 Identities = 145/147 (98%), Positives = 147/147 (100%)

Query: 1   MVHLSGDEKNAVHGLWSKVKVDEVGGEALGRLLVVYPWTRRFFESFGDLSTADAVMNNPK 60
           MV+LSGDEKNAVHGLWSKVKVDEVGGEALGRLLVVYPWTRRFFESFGDLSTADAVMNNPK
Sbjct: 1   MVNLSGDEKNAVHGLWSKVKVDEVGGEALGRLLVVYPWTRRFFESFGDLSTADAVMNNPK 60

Query: 61  VKAHGSKVLNSFGDGLNHLDNLKGTYAKLSELHCDKLHVDPENFRLLGNVLVVVLARHFG 120
           VKAHGSKVLNSFGDGL+HLDNLKGTYAKLSELHCDKLHVDPENFRLLGNVLVVVLARHFG
Sbjct: 61  VKAHGSKVLNSFGDGLSHLDNLKGTYAKLSELHCDKLHVDPENFRLLGNVLVVVLARHFG 120

Query: 121 KEFTPDLQAAYQKVVAGVANALAHRYH 147
           KEFTPDLQAAYQKVVAGVANALAHRYH
Sbjct: 121 KEFTPDLQAAYQKVVAGVANALAHRYH 147
```

sp P18983 **Hemoglobin subunit beta (Hemoglobin beta chain) (Beta-globin) [HBB]** 147 AA
HBB_AILME **[Ailuropoda melanoleuca (Giant panda)]** align

```
 Score =  265 bits (677), Expect = 4e-71
 Identities = 127/147 (86%), Positives = 137/147 (93%)

Query: 1   MVHLSGDEKNAVHGLWSKVKVDEVGGEALGRLLVVYPWTRRFFESFGDLSTADAVMNNPK 60
           MVHL+G+EK AV GLWSKV VDEVGGEALGRLLVVYPWT+RFF+SFGDLST DAVMNNPK
Sbjct: 1   MVHLTGEEKAAVTGLWSKVNVDEVGGEALGRLLVVYPWTQRFFDSFGDLSTPDAVMNNPK 60

Query: 61  VKAHGSKVLNSFGDGLNHLDNLKGTYAKLSELHCDKLHVDPENFRLLGNVLVVVLARHFG 120
           VKAHG KVLNSF +GL +LDNLKGT+AKLSELHCDKLHVDPENF+LLGNVLV VLA HFG
Sbjct: 61  VKAHGKKVLNSFSEGLKNLDNLKGTFAKLSELHCDKLHVDPENFKLLGNVLVCVLAHHFG 120

Query: 121 KEFTPDLQAAYQKVVAGVANALAHRYH 147
           KEFTP +QAAYQKVVAGVANALAH+YH
Sbjct: 121 KEFTPQVQAAYQKVVAGVANALAHKYH 147
```

Ex.5

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Welcome to the SIB BLAST Network Service

If results of this search are reported or published, please mention that
the computation was performed at the SIB using the BLAST network service.
The SIB BLAST network service uses a server developed at SIB and the NCBI
BLAST 2 software.

In case of problems, please read the online BLAST help.
If your question is not covered, please contact <helpdesk@expasy.org>.

NCBI BLAST program reference [PMID:9254694]:
Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W.,
Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein
database search programs. Nucleic Acids Res. 25:3389-3402(1997).

==========

Query: 222 AA (of which 7% low-complexity regions filtered out)
Date run: 2007-02-09 18:08:22 UTC+0100 on blast01.vital-it.ch
Program: NCBI BLASTP 2.2.15 [Oct-15-2006]
Database: UniProtKB Mammalia
240,475 sequences; 91,865,493 total letters
UniProt Knowledgebase Release 9.6 consists of:
UniProtKB/Swiss-Prot Release 51.6 of 06-Feb-2007: 257964 entries
UniProtKB/TrEMBL Release 34.6 of 06-Feb-2007: 3745801 entries

Taxonomic view | NiceBlast view | Printable view

List of potentially matching sequences

Send selected sequences to Clustal W (multiple alignment) Submit Query Select up to...

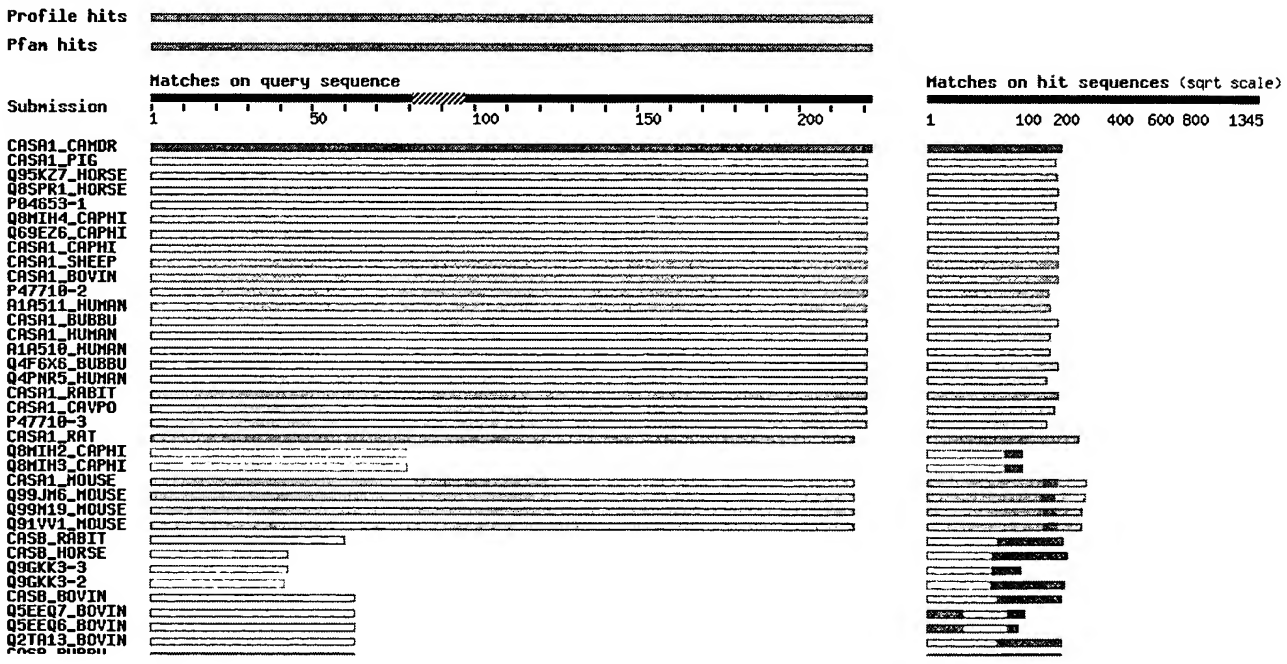
☐ Include query sequence

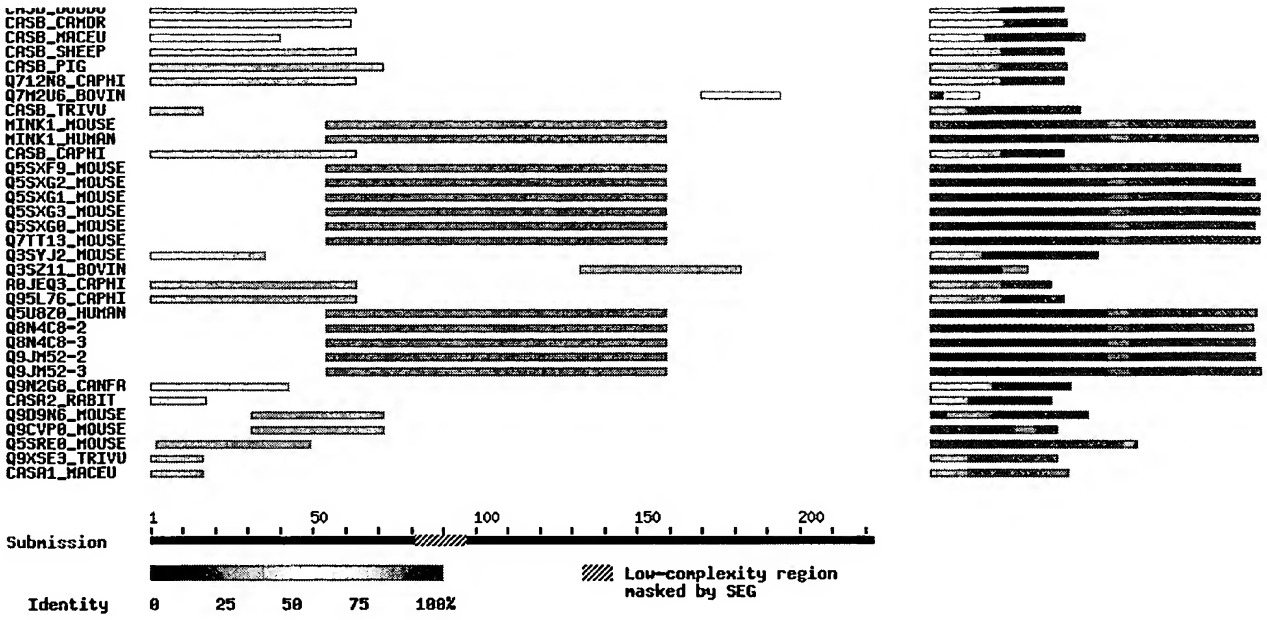
	Db	AC	Description	Score	E-value
☐	sp	O97943	CASA1_CAMDR Alpha-S1-casein precursor [CSN1S1] [Camelu...	418	e-117
☐	sp	P39035	CASA1_PIG Alpha-S1-casein precursor [CSN1S1] [Sus scro...	176	8e-44
☐	tr	Q95KZ7	_HORSE AlphaS1-casein [Equus caballus (Horse)]	146	5e-35
☐	tr	Q8SPR1	_HORSE Alpha s1 casein [Equus caballus (Horse)]	146	5e-35
☐	sp_vs	P04653-1	Isoform 2 of P04653 - Ovis aries (Sheep) [CSN1S1]...	134	3e-31
☐	tr	Q8MIH4	_CAPHI Alpha s1 casein [csn1S1] [Capra hircus (Goat)]	131	2e-30
☐	tr	Q69EZ6	_CAPHI CSCN1 [Capra hircus (Goat)]	130	4e-30
☐	sp	P18626	CASA1_CAPHI Alpha-S1-casein precursor (Alpha-S1-CN) [C...	128	1e-29
☐	sp	P04653	CASA1_SHEEP Alpha-S1-casein precursor [CSN1S1] [Ovis a...	127	3e-29
☐	sp	P02662	CASA1_BOVIN Alpha-S1-casein precursor [CSN1S1] [Bos ta...	126	5e-29
☐	sp_vs	P47710-2	Isoform 2 of P47710 - Homo sapiens (Human) [CSN1S...	126	5e-29
☐	tr	A1A511	_HUMAN Casein alpha s1 [CSN1S1] [Homo sapiens (Human)]	124	2e-28
☐	sp	O62823	CASA1_BUBBU Alpha-S1-casein precursor [CSN1S1] [Bubalu...	123	5e-28
☐	sp	P47710	CASA1_HUMAN Alpha-S1-casein precursor [Contains: Casox...	123	6e-28
☐	tr	A1A510	_HUMAN Casein alpha s1 (Casein alpha s1, isoform CRA_b)...	123	6e-28
☐	tr	Q4F6X6	_BUBBU Alpha-S1 casein [Bubalus bubalis (Domestic water...	120	4e-27
☐	tr	Q4PNR5	_HUMAN Casein [Homo sapiens (Human)]	120	5e-27
☐	sp	P09115	CASA1_RABIT Alpha-S1-casein precursor (Alpha-casein) [...	119	9e-27
☐	sp	P04656	CASA1_CAVPO Alpha-S1-casein precursor (Casein-B) [CSN1...	116	7e-26
☐	sp_vs	P47710-3	Isoform 3 of P47710 - Homo sapiens (Human) [CSN1S...	107	3e-23
☐	sp	P02661	CASA1_RAT Alpha-S1-casein precursor (Alpha-casein) [Cs...	68	3e-11
☐	tr	Q8MIH2	_CAPHI Alpha s1 casein [csn1S1] [Capra hircus (Goat)]	67	5e-11
☐	tr	Q8MIH3	_CAPHI Alpha s1 casein [csn1S1] [Capra hircus (Goat)]	64	3e-10
☐	sp	P19228	CASA1_MOUSE Alpha-S1-casein precursor (Alpha-casein) [...	62	1e-09
☐	tr	Q99JM6	_MOUSE Csn1s1 protein [Csn1s1] [Mus musculus (Mouse)]	62	1e-09
☐	tr	Q99M19	_MOUSE Csn1s1 protein [Csna] [Mus musculus (Mouse)]	54	6e-07
☐	tr	Q91VV1	_MOUSE Csn1s1 protein [Csn1s1] [Mus musculus (Mouse)]	50	8e-06
☐	sp	P09116	CASB_RABIT Beta-casein precursor [CSN2] [Oryctolagus c...	39	0.015
☐	sp	Q9GKK3	CASB_HORSE Beta-casein precursor [CSN2] [Equus caballu...	37	0.073
☐	sp_vs	Q9GKK3-3	Isoform 3 of Q9GKK3 - Equus caballus (Horse) [CSN...	37	0.073
☐	sp_vs	Q9GKK3-2	Isoform 2 of Q9GKK3 - Equus caballus (Horse) [CSN...	36	0.096

☐	sp	P02666	CASB_BOVIN Beta-casein precursor [CSN2] [Bos taurus (B...	35	0.21
☐	tr	Q5EEQ7	_BOVIN Beta-casein (Fragment) [Bos taurus (Bovine)]	35	0.21
☐	tr	Q5EEQ6	_BOVIN Kappa-casein (Fragment) [Bos taurus (Bovine)]	35	0.21
☐	tr	Q2TA13	_BOVIN CSN2 protein [CSN2] [Bos taurus (Bovine)]	35	0.21
☐	sp	Q9TSI0	CASB_BUBBU Beta-casein precursor [CSN2] [Bubalus bubal...	35	0.28
☐	sp	Q9TVD0	CASB_CAMDR Beta-casein precursor [CSN2] [Camelus drome...	33	0.62
☐	sp	P28550	CASB_MACEU Beta-casein precursor [CSN2] [Macropus euge...	32	1.4
☐	sp	P11839	CASB_SHEEP Beta-casein precursor [CSN2] [Ovis aries (S...	32	1.8
☐	sp	P39037	CASB_PIG Beta-casein precursor [CSN2] [Sus scrofa (Pig)]	32	1.8
☐	tr	Q712N8	_CAPHI Beta-casein precursor [csn2] [Capra hircus (Goat)]	32	1.8
☐	tr	Q7M2U6	_BOVIN Alpha-S1-casein (Fragments) [Bos taurus (Bovine)]	32	1.8
☐	sp	Q9XSE4	CASB_TRIVU Beta-casein precursor [CSN2] [Trichosurus v...	32	2.4
☐	sp	Q9JM52	MINK1_MOUSE Misshapen-like kinase 1 (EC 2.7.11.1) (Mit...	31	3.1
☐	sp	Q8N4C8	MINK1_HUMAN Misshapen-like kinase 1 (EC 2.7.11.1) (Mit...	31	3.1
☐	sp	P33048	CASB_CAPHI Beta-casein precursor [CSN2] [Capra hircus ...	31	3.1
☐	tr	Q5SXF9	_MOUSE Mitogen-activated protein kinase kinase kinase k...	31	3.1
☐	tr	Q5SXG2	_MOUSE Mitogen-activated protein kinase kinase kinase k...	31	3.1
☐	tr	Q5SXG1	_MOUSE Mitogen-activated protein kinase kinase kinase k...	31	3.1
☐	tr	Q5SXG3	_MOUSE Mitogen-activated protein kinase kinase kinase k...	31	3.1
☐	tr	Q5SXG0	_MOUSE Mitogen-activated protein kinase kinase kinase k...	31	3.1
☐	tr	Q7TT13	_MOUSE Mink1 protein [Mink1] [Mus musculus (Mouse)]	31	3.1
☐	tr	Q3SYJ2	_MOUSE 4930432K09Rik protein [4930432K09Rik] [Mus muscu...	31	3.1
☐	tr	Q3SZ11	_BOVIN Similar to replication protein A3, 14kDa [MGC128...	31	3.1
☐	tr	A0JEQ3	_CAPHI Beta-casein precursor [csn2] [Capra hircus (Goat)]	31	3.1
☐	tr	Q95L76	_CAPHI Beta-casein precursor [csn2] [Capra hircus (Goat)]	31	3.1
☐	tr	Q5U8Z0	_HUMAN Misshapen/NIKs-related kinase isoform beta [MINK...	31	3.1
☐	sp_vs	Q8N4C8-2	Isoform 1 of Q8N4C8 - Homo sapiens (Human) [MINK1...	31	3.1
☐	sp_vs	Q8N4C8-3	Isoform 2 of Q8N4C8 - Homo sapiens (Human) [MINK1...	31	3.1
☐	sp_vs	Q9JM52-2	Isoform 1 of Q9JM52 - Mus musculus (Mouse) [Mink1...	31	3.1
☐	sp_vs	Q9JM52-3	Isoform 3 of Q9JM52 - Mus musculus (Mouse) [Mink1...	31	3.1
☐	tr	Q9N2G8	_CANFA Beta-casein [Canis familiaris (Dog)]	31	4.0
☐	sp	P50419	CASA2_RABIT Alpha-S2-casein precursor (Alpha-S2B-casei...	30	5.2
☐	tr	Q9D9N6	_MOUSE Adult male testis cDNA, RIKEN full-length enrich...	30	5.2
☐	tr	Q9CVP0	_MOUSE Adult male testis cDNA, RIKEN full-length enrich...	30	5.2
☐	tr	Q5SRE0	_MOUSE Aldehyde dehydrogenase family 3, subfamily A2 [A...	30	6.8
☐	tr	Q9XSE3	_TRIVU Alpha-casein [Trichosurus vulpecula (Brush-taile...	30	6.8
☐	sp	P28549	CASA1_MACEU Alpha-S1-casein precursor (Alpha-casein) [...	30	8.9

Graphical overview of the alignments

Click here to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs
(? Help) (use ScanProsite for more details about PROSITE matches)





Alignments

sp O97943 CASA1_CAMDR **Alpha-S1-casein precursor [CSN1S1] [Camelus dromedarius (Dromedary) (Arabian camel)]** 222 AA align

Score = 418 bits (1074), Expect = e-117
Identities = 206/222 (92%), Positives = 206/222 (92%)

```
Query: 1   MKLLILTCLVAVALARPKYPLRYPEVFQNEPDSIEEVLNKRKILELAVVSPIQFRQENID 60
           MKLLILTCLVAVALARPKYPLRYPEVFQNEPDSIEEVLNKRKILELAVVSPIQFRQENID
Sbjct: 1   MKLLILTCLVAVALARPKYPLRYPEVFQNEPDSIEEVLNKRKILELAVVSPIQFRQENID 60

Query: 61  ELKDTRNEPTEDHIMEDTERKXXXXXXXXXXXXXXXXXQKDILKEDMPSQRYLEELHRLNK 120
           ELKDTRNEPTEDHIMEDTERK                 QKDILKEDMPSQRYLEELHRLNK
Sbjct: 61  ELKDTRNEPTEDHIMEDTERKESGSSSSEEVVSSTTEQKDILKEDMPSQRYLEELHRLNK 120

Query: 121 YKLLQLEAIRDQKLIPRVKLSSHPYLEQLYRINEDNHPQLGEPVKVVTQPFPQFFQLGAS 180
           YKLLQLEAIRDQKLIPRVKLSSHPYLEQLYRINEDNHPQLGEPVKVVTQPFPQFFQLGAS
Sbjct: 121 YKLLQLEAIRDQKLIPRVKLSSHPYLEQLYRINEDNHPQLGEPVKVVTQPFPQFFQLGAS 180

Query: 181 PYVAWYYPPQVMQYIAHPSSYDTPEGIASEDGGKTDVMPQWW 222
           PYVAWYYPPQVMQYIAHPSSYDTPEGIASEDGGKTDVMPQWW
Sbjct: 181 PYVAWYYPPQVMQYIAHPSSYDTPEGIASEDGGKTDVMPQWW 222
```

sp P39035 CASA1_PIG **Alpha-S1-casein precursor [CSN1S1] [Sus scrofa (Pig)]** 206 AA align

Score = 176 bits (445), Expect = 8e-44
Identities = 110/231 (47%), Positives = 128/231 (55%), Gaps = 35/231 (15%)

```
Query: 1   MKLLILTCLVAVALARPKYPLRYPEVFQNEPDSIEEVLNKRKILELAVVSPI-QFRQENI 59
           MKLLI  CL AVALARPK PLR+ E  QNEPDS EE+  +RK L    V  + QFRQE I
Sbjct: 1   MKLLIFICLAAVALARPKPPLRHQEHLQNEPDSREELFKERKFLRFPEVPLLSQFRQEII 60

Query: 60  DELKDTRNEPTEDHIMEDTERKXXXXXXXXXXXXXXXXXQKDILK-EDMPSQRYLEELHRL 118
           +EL         +H ME  E++                QK + K ED+PSQ YL  L  L
Sbjct: 61  NEL-------NRNHGMEGHEQRGSSSSSSEEVVGNSAEQKHVQKEEDVPSQSYLGHLQGL 113

Query: 119 NKYKLLQLEAIRDQKLIPRVKLSSHPYLEQLYRINEDNHPQLGEPVKVVTQ--------P 170
           NKYKL QLEAI DQ               +L+R NED H Q GEP+K V Q         P
Sbjct: 114 NKYKLRQLEAIHDQ---------------ELHRTNEDKHTQQGEPMKGVNQEQAYFYFEP 158

Query: 171 FPQFFQLGASPYVAWYYPPQVMQYIAHPSSYDTPEGIASEDGGKTDVMPQW 221
             QF+QL A PY  WYYPP   QYIAHP   + P+  A E GGKT++MPQW
Sbjct: 159 LHQFYQLDAYPYATWYYPP---QYIAHPLFTNIPQPTAPEKGGKTEIMPQW 206
```

GK

==========

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The SIB BLAST network service uses a server developed at SIB and the NCBI
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If your question is not covered, please contact <helpdesk@expasy.org>.

NCBI BLAST program reference [PMID:9254694]:
Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W.,
Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein
database search programs. Nucleic Acids Res. 25:3389-3402(1997).

==========

Query: 232 AA
Date run: 2007-02-09 18:11:58 UTC+0100 on blast01.vital-it.ch
Program: NCBI BLASTP 2.2.15 [Oct-15-2006]
Database: UniProtKB Mammalia
240,475 sequences; 91,865,493 total letters
UniProt Knowledgebase Release 9.6 consists of:
UniProtKB/Swiss-Prot Release 51.6 of 06-Feb-2007: 257964 entries
UniProtKB/TrEMBL Release 34.6 of 06-Feb-2007: 3745801 entries

Taxonomic view | NiceBlast view | Printable view

List of potentially matching sequences

Send selected sequences to Clustal W (multiple alignment) Submit Query Select up to...

☐ Include query sequence

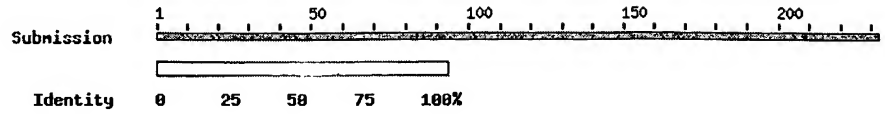
	Db	AC	Description	Score	E-value
☐	sp	Q9TVD0	CASB_CAMDR Beta-casein precursor [CSN2] [Camelus drome...	463	e-130
☐	sp	P39037	CASB_PIG Beta-casein precursor [CSN2] [Sus scrofa (Pig)]	305	7e-83
☐	tr	Q28229	_CAMDR B-casein (Fragment) [Camelus dromedarius (Dromed...	286	4e-77
☐	sp	P11839	CASB_SHEEP Beta-casein precursor [CSN2] [Ovis aries (S...	285	7e-77
☐	sp	Q9TSI0	CASB_BUBBU Beta-casein precursor [CSN2] [Bubalus bubal...	285	1e-76
☐	tr	Q712N8	_CAPHI Beta-casein precursor [csn2] [Capra hircus (Goat)]	282	6e-76
☐	tr	Q95L76	_CAPHI Beta-casein precursor [csn2] [Capra hircus (Goat)]	282	6e-76
☐	sp	P33048	CASB_CAPHI Beta-casein precursor [CSN2] [Capra hircus ...	281	1e-75
☐	sp	P02666	CASB_BOVIN Beta-casein precursor [CSN2] [Bos taurus (B...	281	2e-75
☐	tr	Q9N2G8	_CANFA Beta-casein [Canis familiaris (Dog)]	280	4e-75
☐	tr	Q2TA13	_BOVIN CSN2 protein [CSN2] [Bos taurus (Bovine)]	277	3e-74
☐	sp	P05814	CASB_HUMAN Beta-casein precursor [CSN2] [Homo sapiens ...	268	1e-71
☐	sp	Q9GKK3	CASB_HORSE Beta-casein precursor [CSN2] [Equus caballu...	256	4e-68
☐	sp_vs	Q9GKK3-2	Isoform 2 of Q9GKK3 - Equus caballus (Horse) [CSN...	241	2e-63
☐	tr	A0JEQ3	_CAPHI Beta-casein precursor [csn2] [Capra hircus (Goat)]	237	2e-62
☐	sp	P09116	CASB_RABIT Beta-casein precursor [CSN2] [Oryctolagus c...	222	1e-57
☐	tr	P79231	_PHYCA Beta casein (Fragment) [Physeter catodon (Sperm ...	207	3e-53
☐	tr	Q6PKV3	_BUBBU Beta casein (Fragment) [Bubalus bubalis (Domesti...	205	1e-52
☐	tr	A1E9C8	_BUBBU Beta-casein (Fragment) [CSN2] [Bubalus bubalis (...	202	1e-51
☐	tr	Q27953	_BALPH B-casein (Fragment) [Balaenoptera physalus (Finb...	201	1e-51
☐	tr	A1YT08	_BOSIN Beta-casein (Fragment) [CSN2] [Bos indicus (Zebu)]	198	1e-50
☐	tr	Q3HW31	_BUBBU Beta-casein (Fragment) [beta-casein] [Bubalus bu...	196	6e-50
☐	tr	Q3HW30	_BUBBU Beta-casein (Fragment) [beta-casein] [Bubalus bu...	196	6e-50
☐	tr	Q28355	_DELLE B-casein (Fragment) [Delphinapterus leucas (Belu...	196	6e-50
☐	tr	A1YQZ8	_BOVIN Beta-casein (Fragment) [CSN2] [Bos taurus (Bovine)]	195	1e-49
☐	tr	Q29151	_UNCUN B-casein (Fragment) [Uncia uncia (Snow leopard) ...	181	3e-45
☐	tr	Q27939	_9CETA B-casein (Fragment) [Alces alces (moose)]	179	6e-45
☐	tr	Q28418	_GIRCA B-casein (Fragment) [Giraffa camelopardalis (Gir...	179	1e-44
☐	tr	Q27938	_ANTAM B-casein (Fragment) [Antilocapra americana (Pron...	178	2e-44
☐	tr	Q9BDG5	_BOVIN Beta casein B (Fragment) [bCN B] [Bos taurus (Bo...	176	6e-44
☐	tr	Q29139	_TRANA B-casein (Fragment) [Tragulus napu (Balabac chev...	172	1e-42

☐	tr	P79092	_AILFU Beta casein (Fragment) [Ailurus fulgens (Lesser ...	161	2e-39
☐	tr	Q28401	_EQUGR B-casein (Fragment) [Equus grevyi (Grevy's zebra)]	160	4e-39
☐	tr	Q29136	_TAPIN B-casein (Fragment) [Tapirus indicus (Asiatic ta...	159	8e-39
☐	tr	Q28442	_HIPAM B-casein (Fragment) [Hippopotamus amphibius (Hip...	149	6e-36
☐	sp	P10598	CASB_MOUSE Beta-casein precursor [Csn2] [Mus musculus ...	141	2e-33
☐	tr	Q3TP33	_MOUSE 10 days lactation, adult female mammary gland cD...	141	2e-33
☐	tr	Q8BGL0	_MOUSE 10 days lactation, adult female mammary gland cD...	135	2e-31
☐	tr	Q9TSD5	_BOVIN Beta-casein A2 variant (Fragments) [Bos taurus (...	134	2e-31
☐	tr	A0N0S5	_BUBBU Beta-casein (Fragment) [Bubalus bubalis (Domesti...	133	6e-31
☐	sp	P02665	CASB_RAT Beta-casein precursor [Csn2] [Rattus norvegic...	131	2e-30
☐	tr	Q5YD57	_CAPHI Beta-casein (Fragment) [CSN2] [Capra hircus (Goat)]	128	2e-29
☐	tr	Q5EEQ7	_BOVIN Beta-casein (Fragment) [Bos taurus (Bovine)]	119	7e-27
☐	tr	Q5EEQ6	_BOVIN Kappa-casein (Fragment) [Bos taurus (Bovine)]	110	6e-24
☐	tr	Q28795	_TAYTA B-casein (Fragment) [Tayassu tajacu (Collared pe...	91	3e-18
☐	sp_vs	Q9GKK3-3	Isoform 3 of Q9GKK3 - Equus caballus (Horse) [CSN...	78	3e-14
☐	tr	Q6UN62	_BOSIN Beta-casein variant A2' (Fragment) [Bos indicus ...	73	8e-13
☐	tr	Q6UN63	_BOVIN Beta-casein variant I (Fragment) [Bos taurus (Bo...	72	2e-12
☐	tr	Q155X6	_BOSIN Beta casein (Fragment) [Bos indicus (Zebu)]	65	2e-10
☐	tr	Q155X5	_BOSIN Beta casein (Fragment) [Bos indicus (Zebu)]	63	8e-10
☐	tr	Q7M2U5	_BUBBU Beta-casein (Fragment) [Bubalus bubalis (Domesti...	57	7e-08
☐	sp	Q8WZ42	TITIN_HUMAN Titin (EC 2.7.11.1) (Connectin) (Rhabdomyo...	53	8e-07
☐	sp_vs	Q8WZ42-2	Isoform 2 of Q8WZ42 - Homo sapiens (Human) [TTN] ...	53	8e-07
☐	sp_vs	Q8WZ42-4	Isoform 4 of Q8WZ42 - Homo sapiens (Human) [TTN] ...	53	8e-07
☐	sp_vs	Q8WZ42-7	Isoform 7 of Q8WZ42 - Homo sapiens (Human) [TTN] ...	53	8e-07
☐	sp_vs	Q8WZ42-8	Isoform 8 of Q8WZ42 - Homo sapiens (Human) [TTN] ...	53	8e-07
☐	tr	Q9UCM5	_HUMAN Beta-casein (Fragment) [Homo sapiens (Human)]	53	1e-06
☐	sp	P02817	AMELX_BOVIN Amelogenin, X isoform precursor (Class I a...	52	1e-06
☐	tr	Q861X2	_BOVIN Amelogenin (Fragment) [AMELX] [Bos taurus (Bovine)]	52	1e-06
☐	tr	Q3UH66	_MOUSE CDNA, RIKEN full-length enriched library, clone:...	50	9e-06
☐	tr	Q9JLE9	_RAT GABA-A receptor epsilon-like subunit [Epsilon] [Ra...	49	1e-05
☐	sp_vs	Q8WZ42-5	Isoform 5 of Q8WZ42 - Homo sapiens (Human) [TTN] ...	49	1e-05
☐	tr	Q71S18	_HUMAN Titin (Fragment) [TTN] [Homo sapiens (Human)]	49	2e-05
☐	tr	O35745	_MOUSE Zinc finger protein [Plagl1] [Mus musculus (Mouse)]	48	3e-05
☐	tr	Q3UQR2	_MOUSE 13 days embryo heart cDNA, RIKEN full-length enr...	48	3e-05
☐	tr	Q9JLQ4	_MOUSE Zinc finger protein ZAC1 [Plagl1] [Mus musculus ...	48	3e-05
☐	tr	Q3UQW2	_MOUSE 12 days embryo eyeball cDNA, RIKEN full-length e...	48	3e-05
☐	tr	Q811F2	_MOUSE Wnk2 protein (Fragment) [Wnk2] [Mus musculus (Mo...	47	8e-05
☐	tr	Q8WMK6	_CAPCR Amelogenin X (Fragment) [AMELX] [Capricornis cri...	47	8e-05
☐	sp	Q6PB44	PTN23_MOUSE Tyrosine-protein phosphatase non-receptor ...	46	1e-04
☐	tr	Q8NBB9	_HUMAN CDNA FLJ33731 fis, clone BRAWH2017685, moderatel...	46	1e-04
☐	sp_vs	Q6PB44-2	Isoform 2 of Q6PB44 - Mus musculus (Mouse) [Ptpn2...	46	1e-04
☐	tr	Q18PS0	_HUMAN Zinc finger homeobox protein 4 (ZFH-4) [ZFH-4] [...	46	1e-04
☐	tr	Q8NF45	_HUMAN FLJ00353 protein (Fragment) [FLJ00353] [Homo sap...	45	2e-04
☐	tr	Q86YA8	_HUMAN YLPM1 protein (Fragment) [YLPM1] [Homo sapiens (...	45	2e-04
☐	tr	Q8CHI3	_MOUSE MKIAA0054 protein (Fragment) [Helz] [Mus musculu...	45	2e-04
☐	tr	Q6DFV5	_MOUSE Helicase with zinc finger domain [Helz] [Mus mus...	45	2e-04
☐	tr	Q8BZZ6	_MOUSE 15 days embryo male testis cDNA, RIKEN full-leng...	45	2e-04
☐	tr	Q7YRG0	_CANFA Cardiac titin isoform N2BA (Fragment) [TTN] [Can...	45	2e-04
☐	sp	P42694	HELZ_HUMAN Probable helicase with zinc-finger domain (...	45	3e-04
☐	tr	Q9JLE8	_MOUSE GABA-A receptor epsilon-like subunit [Gabre] [Mu...	45	3e-04
☐	tr	Q9JLE7	_MOUSE GABA-A receptor epsilon-like subunit [Gabre] [Mu...	45	3e-04
☐	tr	Q861X3	_OTOGA Amelogenin (Fragment) [AMELX] [Otolemur garnetti...	45	3e-04
☐	tr	A1L4L4	_HUMAN Helicase with zinc finger [HELZ] [Homo sapiens (...	45	3e-04
☐	tr	Q86UP3	_HUMAN Zinc finger homeodomain 4 protein [ZFHX4] [Homo ...	45	3e-04
☐	sp_vs	Q8CGF7-2	Isoform 2 of Q8CGF7 - Mus musculus (Mouse) [Tcerg...	45	3e-04
☐	tr	Q861X5	_LEMCA Amelogenin (Fragment) [AMELX] [Lemur catta (Ring...	44	4e-04
☐	tr	Q8WU72	_HUMAN CIZ1 protein (CDKN1A interacting zinc finger pro...	44	4e-04
☐	tr	Q5SYW3	_HUMAN CDKN1A interacting zinc finger protein 1 (CDKN1A...	44	4e-04
☐	tr	Q9H868	_HUMAN CDNA FLJ13916 fis, clone Y79AA1000342, moderatel...	44	4e-04
☐	sp	Q9XSE4	CASB_TRIVU Beta-casein precursor [CSN2] [Trichosurus v...	44	5e-04
☐	sp	O60885	BRD4_HUMAN Bromodomain-containing protein 4 (HUNK1 pro...	43	8e-04
☐	tr	Q3UH70	_MOUSE 14 days pregnant adult female placenta cDNA, RIK...	43	8e-04
☐	sp	Q9ESU6	BRD4_MOUSE Bromodomain-containing protein 4 (Mitotic c...	43	0.001
☐	tr	Q7YRG2	_CANFA Cardiac titin isoform N2BA (Fragment) [TTN] [Can...	43	0.001
☐	tr	Q7YRG1	_CANFA Cardiac titin isoform N2BA (Fragment) [TTN] [Can...	43	0.001
☐	tr	Q7YRF5	_CANFA Cardiac titin (Fragment) [TTN] [Canis familiaris...	43	0.001

☐	sp	Q6R0H6	ALEX_MOUSE Protein ALEX (Alternative gene product enco...	42	0.001
☐	tr	Q7YRF9	_CANFA Cardiac titin isoform N2BA (Fragment) [TTN] [Can...	42	0.001
☐	sp	P79149	PININ_CANFA Pinin [PNN] [Canis familiaris (Dog)]	42	0.002

Graphical overview of the alignments

Click here to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs
(Help) (use ScanProsite for more details about PROSITE matches)



Alignments

sp Q9TVD0 CASB_CAMDR **Beta-casein precursor [CSN2] [Camelus dromedarius (Dromedary) (Arabian camel)]** 232 AA align

Score = 463 bits (1192), Expect = e-130
Identities = 232/232 (100%), Positives = 232/232 (100%)

```
Query: 1   MKVLILACRVALALAREKEEFKTAGEALESISSSEESITHINKQKIEKFKIEEQQQTEDE 60
           MKVLILACRVALALAREKEEFKTAGEALESISSSEESITHINKQKIEKFKIEEQQQTEDE
Sbjct: 1   MKVLILACRVALALAREKEEFKTAGEALESISSSEESITHINKQKIEKFKIEEQQQTEDE 60

Query: 61  QQDKIYTFPQPQSLVYSHTEPIPYPILPQNFLPPLQPAVMVPFLQPKVMDVPKTKETIIP 120
           QQDKIYTFPQPQSLVYSHTEPIPYPILPQNFLPPLQPAVMVPFLQPKVMDVPKTKETIIP
Sbjct: 61  QQDKIYTFPQPQSLVYSHTEPIPYPILPQNFLPPLQPAVMVPFLQPKVMDVPKTKETIIP 120

Query: 121 KRKEMPLLQSPVVPFTESQSLTLTDLENLHLPLPLLQSLMYQIPQPVPQTPMIPPQSLLS 180
           KRKEMPLLQSPVVPFTESQSLTLTDLENLHLPLPLLQSLMYQIPQPVPQTPMIPPQSLLS
Sbjct: 121 KRKEMPLLQSPVVPFTESQSLTLTDLENLHLPLPLLQSLMYQIPQPVPQTPMIPPQSLLS 180

Query: 181 LSQFKVLPVPQQMVPYPQRAMPVQAVLPFQEPVPDPVRGLHPVPQPLVPVIA 232
           LSQFKVLPVPQQMVPYPQRAMPVQAVLPFQEPVPDPVRGLHPVPQPLVPVIA
Sbjct: 181 LSQFKVLPVPQQMVPYPQRAMPVQAVLPFQEPVPDPVRGLHPVPQPLVPVIA 232
```

sp P39037 CASB_PIG **Beta-casein precursor [CSN2] [Sus scrofa (Pig)]** 232 AA align

Score = 305 bits (782), Expect = 7e-83
Identities = 156/230 (67%), Positives = 183/230 (79%), Gaps = 2/230 (0%)

```
Query: 1   MKVLILACRVALALAREKEEFKTAGEALESISSSEESITHINKQKIEKFKIEEQQQTEDE 60
           MK+LILAC VALALAR KEE   +GE +ES+SSSEESITHI+K+KIEK K EEQQQTE+E
Sbjct: 1   MKLLILACFVALALARAKEELNASGETVESLSSSEESITHISKEKIEKLKREEQQQTENE 60

Query: 61  QQDKIYTFPQPQSLVYSHTEPIPYPILPQNFLPPLQPAVMVPFLQPKVMDVPKTKETIIP 120
           +Q+KI+ FPQPQ L + +TEPIPYPILPQN LP  Q  V+VP L P+VM   K KETI+P
Sbjct: 61  RQNKIHQFPQPQPLAHPYTEPIPYPILPQNILPLAQVPVVVPLLHPEVMKDSKAKETIVP 120

Query: 121 KRKEMPLLQSPVVPFTESQSLTLTDLENLHLPLPLLQSLMYQIPQPVPQTPMIPPQSLLS 180
           KRK MP  +SP  PF E QSLTLTD E   L LPLLQSLM+QIPQPVPQTPM  PQ LLS
Sbjct: 121 KRKGMPFPKSPAEPFVEGQSLTLTDFE--VLSLPLLQSLMHQIPQPVPQTPMFAPQPLLS 178

Query: 181 LSQFKVLPVPQQMVPYPQRAMPVQAVLPFQEPVPDPVRGLHPVPQPLVPV 230
           L Q KVLPVPQQ+VP+PQR MP QA+L +Q+P+  P++G +PVPQP+ PV
Sbjct: 179 LPQAKVLPVPQQVVPFPQRDMPFQALLLYQDPLLGPLQGFYPVPQPVAPV 228
```

tr Q28229 Q28229_CAMDR **B-casein (Fragment) [Camelus dromedarius (Dromedary) (Arabian camel)]** 141 AA align

Score = 286 bits (732), Expect = 4e-77
Identities = 140/141 (99%), Positives = 140/141 (99%)

```
Query: 65  IYTFPQPQSLVYSHTEPIPYPILPQNFLPPLQPAVMVPFLQPKVMDVPKTKETIIPKRKE 124
           IYTFPQPQSLVYSHTEPIPYPILPQNFLPPLQPAVMVPFLQPKVMDVPKTKETIIPKRKE
Sbjct: 1   IYTFPQPQSLVYSHTEPIPYPILPQNFLPPLQPAVMVPFLQPKVMDVPKTKETIIPKRKE 60

Query: 125 MPLLQSPVVPFTESQSLTLTDLENLHLPLPLLQSLMYQIPQPVPQTPMIPPQSLLSLSQF 184
           MPLLQSPVVPFTESQSLTLTDLENLHLPLPLLQSLMYQIPQP PQTPMIPPQSLLSLSQF
Sbjct: 61  MPLLQSPVVPFTESQSLTLTDLENLHLPLPLLQSLMYQIPQPXPQTPMIPPQSLLSLSQF 120

Query: 185 KVLPVPQQMVPYPQRAMPVQA 205
           KVLPVPQQMVPYPQRAMPVQA
Sbjct: 121 KVLPVPQQMVPYPQRAMPVQA 141
```